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5.1.6
Compugen Ltd
version
- 2004
GenCore (c) 1993
        Copyright
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using sw model - protein search, OM protein

10:30:32 2004, 30, September Run

updates/sec conds (without alignments)

US-09-955-502-1 139 1 MXRXXXCXXXXXX score: Perfect so Sequence: Title

0.5 Gapext BLOSUM62 Gapop 10.0 Scoring table:

389414 of hits satisfying chosen parameters: Total number

389414 segs, 51625971 residues

Searched:

length: 0 length: 2000000000 8 8 9 9 DB DB Minimum Maximum

Post-processing:

Minimum Match 0% Maximum Match 100% Listing first 50 summaries

Issued_Patents_AA:*

'cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
'cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
'cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
'cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
'cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
'cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
'cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:* 40 m 4 m 9 Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	cription
Н	4	34.	1		-09-543-681A-544	equence 5443, A
N	48	4.	0	4	S-09-489-039A-11	equence 11962,
m	47	ო	110	4	8-09-540-236-2859	equence 2859. A
4	46	33.1	$\boldsymbol{\omega}$	4	US-09-328-352-5456	ence 5456, A
ιO	44	H	α	4	S-09-252-991A-233	equence 23355,
9	Э. 4.	4,	$\mathbf{\omega}$	4	S-09-134-000C-6419	equence 6419, A
7	34	4.	IJ	4	-08-178-257-	equence 5, Appl
හ	ю 44	4	(D)	7	S-08-756-317	equence 5, Appl
ס	33	ო	Γ	4	S-09-489-039A-143	equence 14334,
10	31	∾.	214	41	-09-543-681A-4972	equence 4972, A
11	30	÷	യ	4	S-09-252-991A-183	equence 18318,
12	29	ò	S	4	S-09-213-293D-15	equence 15, App
13	29	0	Γ	4	S-09-489-039A-7	equence 7536, A
14	20	Ö	∞	4	S-09-148-545-144	equence 144, Ap
15	29	Ö	α	4	S-09-148-545-20	equence 209, Ap
16	29	0	Φ	4	S-09-339-159B-1	equence 14, App
17	29		\vdash	4	S-09-134-000C-536	equence 5362, A
18	8		\dashv	41	S-09-252-991A-19	equence 19734,
г 6	29	。	φ	ო	S-09-295-186-1	equence 17, App
20	20		<u>~</u>	ന	S-09-460-14	equence 2, Appl
21	29		<u></u>	4,	S-09-895-547-	equence 2, Appl
22	29	0	σ	M	S-09-460-145-	equence 4, Appl
23	29	。	Q)	4	-09-895-547-	equence 4, Appl
24	29	0	-	ጣ	-08-827-208-	equence 3, Appl
25	29	Ö	\vdash	m	-09-500-358-	equence 3, Appl
56	29		\vdash	m	-09-498-80	equence 3, Appl
27	28	0	23	Н	-07-646-531D	equence 5, App

Appl	App.	tent No. 542610	quence 28, App	17, App	16, App	18, App	equence 1	equence 9, Appl	equence 9, Appl	equence 1, Appl	equence 22823,	quence 4928, A	equence 1, Appl	equence 32389,	equence 3, Appl	equence 26556,	equence 9, Appl	equence 4, Appl	equence 14269,	equence 7, Appl	equence 6987, A	equence 18, App
-488-	-197-77	26100-	-152-721B-2	-213-293D-	3-293D-1	-874-832-1	-09-097-233-1	5-08-874-832-	S-09-097-233-	3-08-985-	-09-252-9	US-09-134-000C-4928	T-US93-0165	-09-252-991A-	-08-985-5	-09-252-99	-09-092-636-	-09-092-63	-09-489-03	-09-075-505-7	Ą	5-1
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ALIGNMENTS

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AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI THERAPEUTICS
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34.5%; Score 48; DB 4;
Best Local Similarity 23.6%; Pred. No. 0.001;
Matches 13; Conservative 0; Mismatches .
US-09-543-681A-5443

US-09-543-681A-5443

Sequence 5443, Application US/09543681A

Patent No. 6605709

GENERAL INFORMATION:

APPLICANT: GARY BRETON

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEU

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEU

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEU

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 5443

LENGTH: 93

TYPE: PRT

ORGANISM: Proteus mirabilis

US-09-543-681A-5443
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RESULT 2
US-09-489-039A-11962
US-09-489-039A-11962
'Sequence 11962, Application US/09489039A
'Sequence 11962, Application US/09489039A
'Patent No. 6610836
'GENERAL INFORMATION:
'APPLICANT: Gary Breton et. al
'TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
'TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
'FILE REFERENCE: 2709.2004001
'FILE REFERENCE: 2709.2004001
'CURRENT APPLICATION NUMBER: US/09/489,039A
'CURRENT FILING DATE: 1999-01-29
'PRIOR FILING DATE: 1999-01-29
'NUMBER OF SEQ ID NOS: 14342
'SEQ ID NO 11962
'LENGTH: 107

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SEQUENCES RELATING TO PSEUDOMONAS
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US-09-134-000C-6419
; Sequence 6419, Application US/09134000C
; Patent No. 6617156
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn DOUCEtte-Stamm et al
; TITLE OF INVENTION: BUTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; FILE REFERENCE: 032796-032
; CURRENT FILING DATE: 1998-08-13
; PRIOR FILING DATE: 1997-08-15
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6419
; LENGTH: 180
; LENGTH: 180
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUEN

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THE
FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 23355

LENGTH: 122

TYPE: PRT
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Pred. No. 0.011;
); Mismatches
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US-08-178-257-5
Sequence 5, Application US/08178257
Patent No. 6515205
GENERAL INFORMATION:
APPLICANT: LIEBERGESELL, MATTHIAS
TITLE OF INVENTION: PRODUCTION OF POI NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3518
                                                                                                                                                                                                                            ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355
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US-09-134-000C-6419
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ilarity 42.9%;
Conservative
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Best Local Similarity 30.3%;
Matches 10; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-09-540-236-2859
US-09-540-236-2859; Application US/09540236
Sequence 2859, Application US/09540236
Batent No. 6673910
Jacht No. 100 2005-001
Jacht Nature Piling Date: 2000-04-04
Jacht No. 2859
Jacht No. 2859
LENGTH: 110
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US-09-328-352-5456

Sequence 5456, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 5456

LENGTH: 92
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                                                                             Score 48; DB 4; Le
Pred. No. 0.0012;
); Mismatches 42;
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Pred. No. 0.002;
); Mismatches
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Pred. No. 0.0029
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US-09-252-991A-23355
; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Acinetobacter baumannii -09-328-352-5456
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                              ) ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962
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ilarity 23.6%;
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iilarity 23.6%;
Conservative (
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| Similarity 30.3%;
10; Conservative
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Best Local Similarity
Matches 13; Conser
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13; Conser
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TOPOLOGY:
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Matches 6
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Sequence 5, Application US/08756317

Patent No. 5849894

GENERAL INFORMATION:

APPLICANT: Clemente, Thomas E.

APPLICANT: Mitsky, Timothy A.

TITLE OF INVENTION: Improved Rhodospirillum Rubrum

TITLE OF INVENTION: Poly-B-Hydroxyalkonoate Synthase

NUMBER OF SEQUENCES: 15

CORRESPONDENCE Arnold, White & Durkee

STREET: TX

COUNTRY: USA

CONTY: Houston

STATE: TX

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/756,317

FILING DATE: 25-NOV-1996
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Pred. No. 5.4;
0; Mismatches
                                                Version
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เคล: 9320/206058
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/178,257
FILING DATE: 11-JAN-1994
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/01291
FILING DATE: 15-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9115245.4
FILING DATE: 16-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 9320/206058
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 6714627 CUSH
TELEFAX: A0MINO ACIDS
TELEFAX: A0MINO ACIDS
TELEFAX: A0MINO ACIDS
TELEFAX: AMMINO ACIDS
TYPE: AMMINO ACIDS
TYPE: AMMINO ACIDS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/007,693
FILING DATE: 29-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alcaligenes eutrophus
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42.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein ORIGINAL SOURCE: ORGANISM: Alcaligenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               264 WYCWYLRHTYLONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inear
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-08-756-317-5
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Best Local S
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Sequence 4972, Application US/09543681A;
Sequence 4972, Application US/09543681A;
Patent No. 6605709;
GENERAL INFORMATION:
APPLICANT: GARY BRETON;
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS;
FILE REFERENCE: 2709.1002-001;
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS;
FILE REFERENCE: 2709.1002-001;
CURRENT APPLICATION NUMBER: US 60/128,706;
PRIOR PILING DATE: 1999-04-09;
NUMBER OF SEQ ID NOS: 8344;
SEQ ID NO 4972;
LENGTH: 214
                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gary Breton et. al
STILE OF INVENTION:
TITLE OF INVENTION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2709.2004001
CURRENT FILING DATE: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
TITLE OF INVENTION NUMBER: US 60/117,747
THE OF INVENTION NUMBER: US 60/117,747
TRIES OF SEQ ID NOS: 14342
SEQ ID NO 14334
LENGTH: 571
TYPE: PRI
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Pred. No. 8.7;
0; Mismatches
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16;
   33,062
IR: MOBT:008
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Pred.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 787-1440
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 589 amino acids
TYPE: amino acids
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29.4%;
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Similarity 42.9%;
6; Conservative
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9-543-681A-4972
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-09-955-502-1.top50.rai

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Sequence 7536, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 7536
LENGTH: 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 170;
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US-09-148-545-144

Sequence 144, Application US/09148545

Patent No. 6590075

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: PZ001P1

CURRENT APPLICATION NUMBER: US/09/148,545

CURRENT FILING DATE: 1998-09-04

EARLIER PEPLICATION NUMBER: 60/040,162

EARLIER APPLICATION NUMBER: 60/040,133

EARLIER APPLICATION NUMBER: 60/040,333

EARLIER APPLICATION NUMBER: 60/040,333

EARLIER FILING DATE: 1997-03-07

EARLIER FILING DATE: 1997-05-23

EARLIER FILING DATE: 1997-05-23
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; Sequence 7536, Application US/09489039A
: Patent No. 6610836
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APPLICATION NUMBER: 60
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Best Local S
Matches 5
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US-09-252-991A-18318

Sequence 18318, Application US/09252991A

Fatent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUMBER: US/09/252,991A

CURRENT FILING DATE: 1998-02-18

FRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,190

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 18318

LENGTH: 285

LENGTH: 285
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US-09-213-293D-15
i Sequence 15, Application US/09213293D
j Patent No. 6384299
j GENERAL INFORMATION:
    APPLICANT: GUTIERREZ-ARMENTA, CRISANTO
    APPLICANT: SANZ-BURGOS, ANDRES P.
    APPLICANT: LOPEZ, PAULA S.
    TILLE OF INVENTION: PLANT RETINOBLASTOMA-ASSOCIATED PROTEINS
    FILE REFERENCE: 604-469
    CURRENT APPLICATION NUMBER: US/09/213,293D
    CURRENT PILING DATE: 1998-12-14
    PRIOR FILING DATE: 1996-06-13
    PRIOR FILING DATE: 1996-06-13
    PRIOR FILING DATE: 1997-06-12
    NUMBER OF SEQ ID NOS: 19
    NUMBER OF SEQ ID NOS: 19
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29;
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Pred. No. 36;
2; Mismatches
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Pred. No.
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Best Local Similarity 28.6%;
Matches 4; Conservative
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larity 42.9%;
Conservative
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Best Local Similarity
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ORGANISM: Gallus
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LENGTH: 131
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EARLIER APPLICATION NUMBER: 60/056, 903
EARLIER FILING DATE: 1979-00-22
EARLIER FILING DATE: 1997-00-22
EARLIER APPLICATION NUMBER: 60/056, 814
EARLIER FILING DATE: 1997-00-22
EARLIER FILING DATE: 1997-00-23
EARLIER FILING

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RAPELICATION NUMBER: 60/047,500
ER FILING DATE: 1997-05-23
ER PELING DATE: 1997-05-23
ER FILING DATE: 1997-05-23
ER FILING DATE: 1997-06-23
ER PILING DATE: 1997-06-23
ER APPLICATION NUMBER: 60/047,598
ER FILING DATE: 1997-05-23
ER PILING DATE: 1997-05-23
ER PILING DATE: 1997-05-23
ER PILING DATE: 1997-06-23
ER FILING DATE: 1997-06-23
ER FILING DATE: 1997-06-23
ER FILING DATE: 1997-06-23
ER FILING DATE: 1997-04-11
ER PILING DATE: 1997-04-11
ER PELING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,671
ER PILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,672
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,672
ER FILING DATE: 1997-04-11
ER PILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,671
ER PILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/056,889
ER FILING DATE: 1997-04-11
ER PRILING DATE: 1997-04-11
ER PRILING DATE: 1997-08-22
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,872
ER FILING DATE: 1997-08-22
ER FILING DATE: 199
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APPLICATION NUMBER: 60
FILING DATE: 1997-08-2
APPLICATION NUMBER: 60
         EARLIER
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NEADUL 140-545-209
Sequence 209, Application US/09148545
Patent No. 659075
GENERAL INPORMATION:
APPLICANT' Rosen et al.
TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: PZ001P1
CURRENT FILING DATE: 1998-03-04
EBARLIER APPLICATION NUMBER: 60/040,162
EBARLIER PILING DATE: 1997-03-07
EBARLIER PILING DATE: 1997-03-07
EBARLIER PILING DATE: 1997-03-07
EBARLIER PILING DATE: 1997-03-07
EBARLIER FILING DATE: 1997-03-07
EBARLIER FILING DATE: 1997-03-07
EBARLIER FILING DATE: 1997-03-07
EBARLIER PILING DATE: 1997-05-23
EBARLIER APPLICATION NUMBER: 60/047,503
EBARLIER PILING DATE: 1997-05-23
EBARLIER PILING DATE: 1997-05-23
EBARLIER APPLICATION NUMBER: 60/047,503
EBARLIER APPLICATI
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Pred. No. 98;
0; Mismatches
  EARLIER FILING DATE: 1997-08-22

EARLIER APPLICATION NUMBER: 60/048,964

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/057,650

EARLIER APPLICATION NUMBER: 60/056,884

EARLIER APPLICATION NUMBER: 60/056,884

EARLIER FILING DATE: 1997-08-22

NUMBER OF SEQ ID NOS: 280

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 144
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5; Conservative
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EARLIER PILING DATE: 1997-08-22

BARLIER PILING DATE: 1997-08-23

BARLIER PILING DATE: 1997-08-28

BARLIER PILING DATE: 1997-08-28
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Sequence 5362, Application US/09134000C;
Patent No. 6617156;
GENERAL INFORMATION:
TITLE OF INVENTION:
THERAPECTICS AND THERAPEUTICS
THERAPECTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 488;
                                                                                                                                                              Length 483;
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                                                                                                                                                              DB 4;
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Sequence 14, Application US/09339159B

Patent No. 6566114

GENERAL INFORMATION:

APPLICANT: Schulein, Markus

APPLICANT: Schnorr, Kirk

APPLICANT: Andersen, Lene

APPLICANT: Andersen, Lene

APPLICANT: Bjornvad, Mads

TITLE OF INVENTION: No. 6566114el Mannanases

FILE REFERENCE: 5440.204-US

CURRENT APPLICATION NUMBER: US/09/339,159B

CURRENT FILING DATE: 1999-06-24

NUMBER OF SEQ ID NOS: 55

SOFTWARE: PatentIn version 3.1

SEQ ID NO 14

LENGTH: 488
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Pred. No. 99;
0; Mismatches
                                                                                                                                                        Score 29; DB Pred. No. 98; 0; Mismatches
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llarity 44.4%;
Conservative
                                                                                                                                                        Query Match
Best Local Similarity 35.7%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                       224 WDRWVRNQANLDKE 237
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NUMBER OF SEQ ID NOS: 280
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 209
LENGTH: 483
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Best Local Similaríty
Matches 4; Conser
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Best Local Similarity
Matches 5; Conser
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SEQ ID NO 5362
LENGTH: 511
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ORGANISM: 1
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COUNTRY: US
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; TOPOLOGY: line
; MOLECULE TYPE: F
US-09-460-145-2
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                                                                                                                                      COUNTRY:
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                                                                                             APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 19734
LENGTH: 519
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US-09-295-186-17
Sequence 17, Application US/09295186B
Patent No. 6127137
GENERAL INFORMATION:
APPLICANT: Hasida, Miyoko
APPLICANT: Tsutsumi, No. 6127137iko
APPLICANT: Halkier, Torben
APPLICANT: Halkier, Torben
TITLE OF INVENTION: An Acidic Phospholipase, Production, and
TITLE OF INVENTION: Methods of Using Thereof (As Amended)
FILE REFERENCE: 4953.204-US
CURRENT APPLICATION NUMBER: 1215/96
PRIOR FILING DATE: 1996-10-31
PRIOR FILING DATE: 1996-10-31
PRIOR FILING DATE: 1997-10-30
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 519;
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RESULT 18
US-09-252-991A-19734
US-09-252-991A-19734, Application US/09252991A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47
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Patent No. 6287838
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                             20.9%;
larity 20.0%;
Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 5; Conser
                                           Sequence 19734, Appl. Patent No. 6551795 GENERAL INFORMATION: APPLICANT: Marc J.
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US-09-460-145-2
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Gaps
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Song, Chuanzheng

TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
APPLICANT: Kriz, Ron
APPLICANT: Song, Chuanzheng
TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: '87 CambridgePark Drive
CITY: Cambridge
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 778;
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/895,547

FILING DATE: 29-Jun-2001

CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 29; DB 3; Le
Pred. No. 1.5e+02;
); Mismatches 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08/788,975
                                                                                                                                                                                                                                                                                                                                                                  CURRENT AFFLICATION DATE:
CLASSIFICATION NUMBER: US/09/460
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/788,97;
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GI52/
TELEPHONE: (617) 498-824
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 778 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 21
US-09-895-547-2
; Sequence 2, Application US/09895547
; Patent No. 6482625
; GENERAL INFORMATION:
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Best Local Similarity 35.7%;
Matches 5; Conservative
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Gaps

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APPLICANT: Kriz, Ron
Song, Chuanzheng
TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridge
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/895,547
FILING DATE: 29-Jun-2001
CLASSIFICATION DATA:
APPLICATION NUMBER: 09/460,145
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REGISTRATION NUMBER: GI5289
TELECOMMUNICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT ON THE OFFICE A.
REGISTRATION NUMBER: GI5289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 797
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                                             Indels
       Length
   Score 29; DB 3; Le
Pred. No. 1.6e+02;
); Mismatches 9;
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Pred. No. 1.6e+02;
; Mismatches 9
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US-08-827-208-3
; Sequence 3, Application US/08827208
; Patent No. 6025178
; GENERAL INFORMATION:
; APPLICANT: Chiou, Xue-Chiou C.
; APPLICANT: Kramer, Ruth M.
; APPLICANT: Sharp, John D.
; APPLICANT: Sharp, John D.
; APPLICANT: Strifler, Beth A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 797 amino acids
TYPE: amino acid
                                                                                                                                                                                                                     Sequence 4, Application US/09895547
Patent No. 6482625
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: <Unknown>
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ilarity 35.7%;
Conservative
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ilarity 35.7%;
Conservative
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ULE TYPE: protein
NCE DESCRIPTION: $
                                                                                     52
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                                                                                    39 WXXWXXXQTXLXNE
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       Query Match
Best Local Similarity
Matches 5; Conser
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Best Local Similarity
Matches 5; Conser
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MOLECULE

SEQUENCE

US-09-895-547-4
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US-09-895-547-4
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APPLICANT: Kriz, Ron
APPLICANT: Kriz, Ron
APPLICANT: Song, Chuanzheng
TITLE OF INVENTION: CYTOSOLIC PHOSPHOLIPASE A2-BETA ENZYMES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE SISTEMATICS INSTITUTE, INC.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: O2140
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/460,145
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US/09/460,145
FILING DATE:
CLASSIFICATION NUMBER: 08/788,975
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GISS89
                                                                                                                                                                                                                                                                                                                                                                                                     778;
                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                    Score 29; DB 4; Le
Pred. No. 1.5e+02;
0; Mismatches 9;
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/460,145
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15289
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEPHONE: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 778 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                   STRANDEDNESS: <Unknown>
;
TOPOLOGY: linear
;
MOLECULE TYPE: protein
;
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-895-547-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09460145
Patent No. 6287838
GENERAL INFORMATION:
APPLICANT: Kriz, Ron
APPLICANT: Song, Chuanzheng
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TELEPHONE: (617) 498-824
TELEFAX: (617) 876-5851
IFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 35.7%;
Matches 5; Conservative
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TYPE:
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TOPOLOGY: 1
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us-09-955-502-1.top50.rai

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RESULT 26
US-09-498-809-3
Sequence 3, Application US/09498809
Patent No. 624206
Jatent Ramer, Ruth M.
APPLICANT: Sharp, John D.
JAPLICANT: Strifler, Beth A.
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
JADRESSEE: Bil Lilly and Company
STREET: Lilly Corporate Center
CITY: Indiana
COUNTY: United States of America
JIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: BAPELICATION DATE:
JAPPLICATION NUMBER: US/09/498,809
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 913;
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Version #1.30
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Pred. No. 1.8e+02;
; Mismatches 9;
                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/827,208
FILING DATE: 28-MAR-1997
APPLICATION NUMBER: US 60/014,608
FILING DATE: 29-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,264
FILING DATE: 19-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: X-10610
TELECOMMUNICATION INFORMATION:
TELEFAX: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,264
FILING DATE: 19-MAR-1997
ATTORNEY/AGENT INFORMATION:
                                        US/09/500,358
 Release #1.0,
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Best Local Similarity 35.7%;
Matches 5; Conservative
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amino acid
iY: linear
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SOFTWARE: Patentin ReCURRENT APPLICATION NUMBER: UFILING DATE:
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MOLECULE TYPE:

US-09-500-358-3
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Sequence 3, Application US/09500358

Patent No. 6197569

GENERAL INFORMATION:
APPLICANT: Chiou, Xue-Chiou C.
APPLICANT: Kramer, Ruth M.
APPLICANT: Sharp, John D.
APPLICANT: Strifler, Beth A.
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 AND RELATED
TITLE OF INVENTION: NUCLEIC ACID COMPOUNDS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indiana
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 913;
  HUMAN PHOSPHOLIPASE A2 AND RELATED NUCLEIC ACID COMPOUNDS
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Pred. No. 1.8e+02;
0; Mismatches 9;
                                                                                                                                                                                        ZIP: 46285

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,208
FILING DATE: 28-MAR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/014,608
FILING DATE: 29-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,264
FILING DATE: 19-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: X-10610
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEPAX: (317) 276-0756
TELEPAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                  United States of America
                                                                             ADDRESSEE: Eli Lilly and Company STREET: Lilly Corporate Center CITY: Indianapolis STATE: Indiana COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 35.7%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 913 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 WXXWXXXQTXLXNE 52
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 TITLE OF INVENTION: HITLE OF INVENTION: NINDER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE:
US-08-827-208-3
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US-09-500-358-3
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Patent No. 6339062

GENERAL INFORMATION:
APPLICANT: Tuszynski, George
APPLICANT: Williams, Taffy
APPLICANT: Actor, Paul
TITLE OF INVENTION: RETROINVERSO POLYPEPTIDES THAT MIMIC OR
TITLE OF INVENTION: THROMBOSPONDIN ACTIVITY
FILE REFERENCE: 07206-0021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                  Sequence 5, Application US/08488273

Patent No. 5840692

GENERAL INFORMATION:

APPLICANT: Deutch, Alan H.

APPLICANT: Tuszynski, George P.

TITLE OF INVENTION: THROMBOSPONDIN

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.

STREET: 1601 Market Street, 36th Floor

CITY: Philadelphia

STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                         COUNTRY: USA

ZIP: 19103-2398

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,273
FILING DATE: 19-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/359,263
FILING DATE: 20-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/896,527
FILING DATE: 20-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/896,527
FILING DATE: 22-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 9598-2U4
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 567-2991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
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Pred. No.
              Application US/08488273
5840692
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WXXWXXXQTXLXN 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-488-273-5
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4; Conserv
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US-09-197-770B-11
                                                                                                                                                                                                                                                               COUNTRY:
ZIP: 191
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Best Local S
Matches 4
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Sequence 5, Application US/07646531D

Patent No. 5200397

GENERAL INFORMATION:

APPLICANT: Deutch, Alan Howard

APPLICANT: Tuszynski, George Paul

TITLE OF INVENTION: Thrombospondin

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: W. R. Grace & Co.-Conn.

STREET: 7379 Route 32

CITY: Columbia

STATE: Maryland

COUNTRY: USA

ZIP: 21044

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: Mord Perfect 5.0

CURRENT APPLICATION DATA:

ADDRESSEE: Word Perfect 5.0

CURRENT APPLICATION DATA:

ADDRESSEE: Word Perfect 5.0

CURRENT APPLICATION DATA:

ADDRESSEE: Word Perfect 5.0
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Pred. No. 1.8e+02;
); Mismatches 9;
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Pred. No. 9.5;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/07/646,531D
FILING DATE: 19910131
ATTORNEY/AGENT INFORMATION:
NAME: Appleby, Vanessa L.
REGISTRATION NUMBER: 33223
REFERENCE/DOCKET NUMBER: 01-7896
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 531-4515
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/07/646,531D
                                                              -10610
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-106
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 913 amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-498-809-3
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Best Local Similarity 35.7%;
Matches 5; Conservative
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; MOLECULE TYPE:
US-07-646-531D-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 28
US-08-488-273-5
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Best Local
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US-07-646
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Pred. No. 48;
; Mismatches
APPLICATION NUMBER: US/08/152,721B
FILING DATE: 15-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pasternack Esq., Sam
REGISTRATION NUMBER: 29,576
REFERENCE/DOCKET NUMBER: 181411-011DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-5000
TELEFAX: (617) 248-4000
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 71 amino acids
TVDE: SEQUENCE SEGIO
                                                                                                                                                                                                                                                                                                                                                                                                           Score 28; DB Pred. No. 27; O; Mismatches
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US-09-213-293D-16
; Sequence 16, Application US/09213293D
; Patent No. 6384299
; GENERAL INFORMATION:
; APPLICANT: GUTIERREZ-ARMENTA, CRISANT
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Best Local Similarity 42.9%;
Matches 6; Conservative
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Best Local Similarity 42.9%;
Matches 6; Conservative
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HYPOTHETICAL: NO
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
IMMEDIATE SOURCE:
CLONE: RB region 6
US-08-152-7218-28
                                                                                                                                                                                                                                                                                                                            internal
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                                                                                                                                                                                                                                           single
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US-09-213-293D-17
                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sin
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US-08-152-721B-28
; Sequence 28, Application US/08152721B
; Patent No. 5962315
; GENERAL INFORMATION:
; APPLICANT: Livingston, David M.
; APPLICANT: Ewen, Mark E.
; TITLE OF INVENTION: Related Polypeptides
; TITLE OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CHOATE, HALL & STEWART
; STREET: 53 State Street
; CITY: Boston
                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 23
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                                                                                                                                     FEATURE:
CTHER INFORMATION: Description of Artificial Sequence:
CTHER INFORMATION: fragment/analog of thrombospondin
US-09-197-770B-11
                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                          RESULT 30
5426100-5
;Patent No. 5426100
; APPLICANT: DEUTCH, ALAN H.;TUSZYNSKI, GEORGE
; TITLE OF INVENTION: PIPTIDE FRAGMENTS AND ANALOGS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: MA

COUNTRY: USA

ZIP: 02109-2891

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
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Pred. No. 9.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ore 28; DB 6 ed. No. 9.5; Mismatches
CURRENT APPLICATION NUMBER: US/09/197,770B
CURRENT FILING DATE: 1998-11-23
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 23
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/110,146
FILING DATE: 20-AUG-1993
PRIOR APPLICATION DATA:
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FILING DATE: 09-JUN-1992
APPLICATION NUMBER: 483,527
FILING DATE: 22-FEB-1990
SEQ ID NO:5:
LENGTH: 23
                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.1%;
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Best Local Similarity 30.8%;
Matches 4; Conservative
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Best Local Similarity 30.8
Matches 4; Conservative
                                                                                                                                                                                                                                                                                          39 WXXWXXXQTXLXN
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US-09-213-293D-17
Sequence 17, Application US/09213293D
Patent No. 6384299
GENERAL INFORMATION:
APPLICANT: GUTIERREZ-ARMENTA, CRISANTO
APPLICANT: SANZ-BURGOS, ANDRES P.
APPLICANT: LOPEZ, PAULA S.
TITLE OF INVENTION: PLANT RETINOBLASTOMA-ASSOCIATED PROTEINS
FILE REFERENCE: 604-469
CURRENT APPLICATION NUMBER: US/09/213,293D
CURRENT APPLICATION NUMBER: PCT/ES96/00130
PRIOR FILING DATE: 1996-06-13
PRIOR FILING DATE: 1996-06-13
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 17
LENGTH: 130
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Indels
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AND METHODS
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                                    Length 178;
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                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/097,233

FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         3: David A. Jackson, Esq.
411 Hackensack Ave, Continental Plaza,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ະບ
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Pred. No. 65;
0; Mismatches
                                    DB
65;
                                                        d. No. 65;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 2261-1-001 N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            z
                                                                                                                                                        US-09-097-233-18

Sequence 18, Application US/09097233

Patent No. 6020162

GENERAL INFORMATION:
APPLICANT: Burley, Stephen K.
APPLICANT: Sonenberg, Nahum
APPLICANT: Marcotrigiano, Joseph
APPLICANT: Gingras, Anne-Claude
TITLE OF INVENTION: A CRYSTAL OF A PI
TITLE OF INVENTION: A CRYSTAL OF A PI
TITLE OF INVENTION: USE THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
                                    Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-874-832-9
; Sequence 9, Application US/08874832
; Patent No. 5872011
; GENERAL INFORMATION:
; APPLICANT: Burly, Stephen K.
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4; Conservative
                                     20.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acids
TYPE: amino acid
                                                                         Conservative
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                                                     Similarity
4; Conserv
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                                                                                                                                             8 WTFWYDIOT
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                                                                                                           39 WXXWXXQT
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                                                                                                                                                                                                     RESULT 35
US-09-097-233-18
  US-08-874-832-18
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Best Local S
Matches 4
                                    Query Match
Best Local S
Matches 4
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Sequence 18, Application US/08874832

Patent No. 5872011

GENERAL INFORMATION:

APPLICANT: Burly, Stephen K.

APPLICANT: Sonenberg, Nahum

APPLICANT: Marcotrigiano, Joseph

APPLICANT: Marcotrigiano, Joseph

APPLICANT: Marcotrigiano, Joseph

TITLE OF INVENTION: A CRYSTAL OF A PROTEIN-LIGAND COMPLEX

TITLE OF INVENTION: CONTAINING AN N-TERMINAL TRUNCATED eIF4E, P

TITLE OF INVENTION: USE THEREOF

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: David A. Jackson, Esq.

STREET: Floor

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

STATE: O7601

CONTENT: DANA
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0
                                                                                                                                                                                                                                                                                                                                                   Length 131;
                                                                                                                                                                                                                                                                                                                                                                                       Indels
APPLICANT: SANZ-BURGOS, ANDRES P.
APPLICANT: XIE, QI
APPLICANT: LOPEZ, PAULA S.
IITLE OF INVENTION: PLANT RETINOBLASTOMA-ASSOCIATED PRO
CURRENT APPLICATION NUMBER: US/09/213,293D
CURRENT FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: PCT/ES96/00130
PRIOR FILING DATE: 1996-06-13
PRIOR FILING DATE: 1997-06-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/874,832
FILING DATE: 13-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 226,742
REFERENCE/DOCKET NUMBER: 226,742
REFERENCE/DOCKET NUMBER: 2261-1-001
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
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Pred. No. 49;
0; Mismatches
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42.9%;
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 42.8
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 WTLFOHTLONEYEL
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                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Mus
US-09-213-293D-16
                                                                                                                                                                                                                     SOFTWARE: Pat
SEQ ID NO 16
LENGTH: 131
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US-08-874-832-18
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Best Local Similarity
Matches 4; Conser
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HYPOTHETICAL:

US-09-097-233-9
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US-08-985-526-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGIH:
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US-09-097-233-9
i Sequence 9, Application US/09097233
j Patent No. 6020162
j Fatent No. 6020162
j GENERAL INFORMATION:
i APPLICANT: Burley, Stephen K.
papplicant: Gonenberg, Nahum
papplicant: Gonenberg, Nahum
papplicant: Gonenberg, Nahum
papplicant: Gontainent OF A PROTEIN-LIGAND COMPLEX
papplicant: Gontainent OF A PROTEIN-LIGAND COMPLEX
print OF INVENTION: USE THEREOF
print OF SEQUENCES: 18
print 
APPLICANT: Sonenberg, Nahum
APPLICANT: Marcotrigiano, Joseph
APPLICANT: Gingras, Anne-Claude
TITLE OF INVENTION: A CRYSTAL OF A PROTEIN-LIGAND COMPLEX
TITLE OF INVENTION: USE THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
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SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/874,832

FILING DATE: 13-JUN-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 2261-1-001

TELEFONMUNICATION INFORMATION:

TELEFAX: 201-487-5800

TELEFAX: 201-487-5800

TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 209 amino acids

TYPE: amino acid
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Pred. No. 76;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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4; Conservative
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MEDIUM TYPE: Floppy disk
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HYPOTHETICAL: 1-08-874-832-9
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Best Local S
Matches 4
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ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE
THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,233
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 2261-1-001 N
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Version #1.25
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ed. No. 76;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KESULT 38
US-08-985-526-1
; Sequence 1, Application US/08985526
; Patent No. 6080728
; GENERAL INFORMATION:
    TITLE OF INVENTION: CARRIER: DNA COMPLE;
    TITLE OF INVENTION: THERAPY
    TITLE OF INVENTION: THERAPY
; TITLE OF INVENTION: THERAPY
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
    ADDRESSEB: Connolly, Bove, Lodge, &;
    STREET: 1220 Market Street, P.O. Box
CITY: Wilmington
    STATE: Delaware
    COUNTRY: U.S.A.
    ZIP: 19899
    COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    COMPUTER: IBM PC compatible
    COMPUTER: IBM PC compatible
    COMPUTER: BATENIN SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIN Release #1.0, Veri
    CURRENT APPLICATION DATA:
    APPLICATION: TAND.
    CLASSIFICATION: TAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 28;
Pred. No.
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APPLICATION NUMBER: US 08/608,845
FILING DATE: 16-JUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: McMorrow Jr., Robert G
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 658-9141
TELEFAX: (302) 658-5613
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.1%;
ilarity 44.4%;
Conservative
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NO
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                                                                                                                                                                                                                                                                                                                     Version #1.25
Sequence 1, Application PC/TUS>SOLODE
GENERAL INFORMATION:
APPLICANT: Bouck, Noel P.
APPLICANT: Polverini, Peter J.
APPLICANT: Good, Deborah J.
APPLICANT: Frazier, William A.
TITLE OF INVENTION: Method and Composition for TITLE OF INVENTION: Inhibiting Angiogenesis
TITLE OF INVENTION: Inhibiting Angiogenesis
TITLE OF SEQUENCES: 12
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                                                                                                                                                                Lungmus & C
cive, Suite
                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01652
FILING DATE: 19930222
CLASSIFICATION:
APPLICATION NUMBER: US/07/841,656
FILING DATE: 24-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/464,369
FILING DATE: 12-JAN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Fentress, Susan B.
REGISTRATION NUMBER: 31,327
REFERENCE/DOCKET NUMBER: 92005-PCT
TELEPHONE: (312)-456-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 28;
Pred. No.
                                                                                                                             NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tilton, Fallon, Lung
STREET: 100 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 239 amin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 239 amino acids
AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                          STREET: 100 South CITY: Chicago STATE: Illinois COUNTRY: USA ZIP: 60606-4002 COMPUTER READABLE FO MEDIUM TYPE: Flow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 4; Conserv
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TOPOLOGY: unk
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Best Local S
Matches 4
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Sequence 4928, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: BNTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPE
FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Patentin version 3.1
                                                                                                                                                           RESULT 39
US-09-252-991A-22823
; Sequence 22823, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATI:
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS;
; TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS;
; TITLE OF ILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22823
; SEQ ID NO 22823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 234;
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                         Length 218
                                                       Indels
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                         Score 28; DB : Pred. No. 79; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22823
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illarity 29.4%;
Conservative
                      20.1%;
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Best Local Similarity 44.4%;
Matches 4; Conservative
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          Query Match
Best Local Similarity 30.0
                                                                                                                  85 WSEWTSCSTSCGN
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Best Local Similarity
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US-09-134-000C-4928
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LENGTH: 234
TYPE: PRT
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PCT-US93-01652-1
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ORGANISM:
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ore 28; DB 4;
ed. No. 1.6e+02;
Mismatches 11
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26556
LENGTH: 450
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Pred. No.
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ilarity 23.5%;
Conservative
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Best Local Similarity 30.8%;
Matches 4; Conservative
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Best Local Similarity 30.8%;
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-092-636-9
                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Pseudomonas
US-09-252-991A-26556
                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 4; Conser
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; TYPE: PRT
; ORGANISM: Rattus
US-09-092-636-4
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US-09-092-636-9
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US-09-092-636-4
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                                                                                                                                                                                                                                                                                                                                            James A
CARRIER: DNA COMPLEXES CONTAINING DNA
ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE
THERAPY
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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US-09-252-991A-26556

; Sequence 26556, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELAT.

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136
                                                                                                                             0
                                                                                           Length 389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 441;
                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mixson, James A
TITLE OF INVENTION: CARRIER: DNA COMPLEXES CONTAINING
TITLE OF INVENTION: THERAPY
ITTLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Connolly, Bove, Lodge, & Hutz
STREET: 1220 Market Street, P.O. Box 2207
CITY: Wilmington
STATE: Delaware
COUNTRY: U.S.A.
ZIP: 19899
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                          Score 28; DB 4; Lu
Pred. No. 1.4e+02;
2; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 28; DB 3; Le
Pred. No. 1.5e+02;
); Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,845
FILING DATE: 16-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: MCMOSTOW Jr., Robert G
TELEPHONE: (302) 658-9141
TELEPHONE: (302) 658-5613
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/985,526
                                                                                                                                                                                                                                                                     US-08-985-526-3
; Sequence 3, Application US/08985526
; Patent No. 6080728
; GENERAL INFORMATION:
; APPLICANT: Mixson, James A

j. LENGTH: 389
j. TYPE: PRT
j. ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32389

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                                                                                          Query Match
Best Local Similarity 28.6%;
Matches 4; Conservative
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Best Local Similarity 30.8%;
Matches 4; Conservative
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FILING DATE:
CLASSIFICATION:
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                                                                                                                                                                                            Sequence 9, Application US/09092636A
; Batent No. 6162641
; GENERAL INFORMATION:
; APPLICANT: Goldman, Daniel
; TITLE OF INVENTION:
; FILE REFERENCE: UMI-003
; CURRENT APPLICATION NUMBER: US/09/092,636A
; CURRENT FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09092636A

Patent No. 6162641

GENERAL INFORMATION:

APPLICANT: Goldman, Daniel

APPLICANT: Sapru, Mohan K.

TITLE OF INVENTION: Neuregulin Response Element and FILE REFERENCE: UMI-003

CURRENT APPLICATION NUMBER: US/09/092,636A

CURRENT FILING DATE: 1998-06-05

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 4

LENGTH: 470
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Pred. No. 1.6e+02;
; Mismatches 8;
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Pred. No. 1.6e+02;
1; Mismatches 8;
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17

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GENCEL 3-3-681A-6987

| Sequence 6987, Application US/09543681A
| GENERAL INFORMATION:
| APPLICANT: GARY BRETON
| TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
| CURRENT APPLICATION NUMBER: US 60/128,706
| PRIOR APPLICATION NUMBER: US 60/128,706
| PRIOR FILING DATE: 1999-04-09
| NUMBER OF SEQ ID NOS: 8344
| SEQ ID NO 6987
| TYPE: PRI
| TYPE: PRI
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1; Mismatches
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US-09-295-186-18
; Sequence 18, Application US/09295186B
; Patent No. 6127137
; GENERAL INFORMATION:
; APPLICANT: Hasida, Miyoko
; APPLICANT: Halkier, Torben
; APPLICANT: Stringer, Mary Ann
; TITLE OF INVENTION: An Acidic Phospholipase, Pro
; TITLE OF INVENTION: Methods of Using Thereof
; FILE REFERENCE: 4953.204-US
; CURRENT APPLICATION NUMBER: US/09/295,186B
; CURRENT FILING DATE: 1999-04-20
; PRIOR APPLICATION NUMBER: 1215/96
; PRIOR FILING DATE: 1997-10-30
; WUMBER OF SEQ ID NOS: 18
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 649
           Score 28; DB 4;
Pred. No. 1.9e+02
); Mismatches
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          Similarity 42.9%; 6; Conservative
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                                                                                            Sequence 14269, Application US/09489039A
; Sequence 14269, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATI
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS;
; TITLE OF INVENTION: NUMBER: US/09/489, 039A
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 14269
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
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Pred. No. 1.8e+02;
0; Mismatches 5;
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TYPE: amino acid
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Minimum Maximum Maximum

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2: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5 ABB78169 5 ABB78177 5 ABB78176 5 ABB78149	ABB7817 ABB7817 ABB7814 ABB7816	ABB7817 ABB7817 ABB7045	AAR1068 AAR3219 AAE1089	ABU1099 ABU1097 ABU1097 ABU1098	ABU1097 ABU1098 ABU1096	ABU1098 ABU1098 ABU1098 ABU1098
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ALIGNMENTS

enterica serovar typhimurium; Salmonella en' YggX homologue a YggX homologue. AA ი 0 cell; YggX; DNA damage; 2000US-0234588P 18-SEP-2001; 2001US-00955502 ABB78165 standard; protein; entry) 당 (first segnence Superoxide damage; hydroxyl radical; I US2002072118-A1 22-SEP-2000; Unidentified 05-NOV-2002 13-JUN-2002 Amino acid ABB78165; RESULT 1 ABB78165

Gralnick JA; ď WPI; 2002-589476/63 (DOWN/) DOWNS D. (GRAL/) GRALNICK J Downs D,

Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant cell, comprises engineering the cell to produce more YggX protein, a protein identified from Salmonella enterica Serovar Typhimurium.

Example, Fig 1A; 16pp; English

The specification describes a method for reducing superoxide damage to a cell. The method comprises engineering the cell to produce more than the native amount of YggX protein (a protein identified from Salmonella enterica serovar typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YggX reduces the oxidation of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer

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useful for
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useful
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NA damage; YggX homologue.
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in a bacterial, yeast,
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                                                    35.3%; Score 49; DB 5;
larity 23.6%; Pred. No. 0.0023;
Conservative 0; Mismatches 4.
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GRALNICK J A.
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radical; DNA damage; YggX homologue.
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GRALNICK J
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protein identified from Salmonella enterica Serovar Typhimur
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Reducing superoxide damage to a cell, e.g. bacterial, mammalian or cell, comprises engineering the cell to produce more YggX protein, protein identified from Salmonella enterica Serovar Typhimurium.
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                  Sequence
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cell.
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ABB7815
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                                                                             typhimurium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         le damage; cell; YggX; Salmonella enterica serovar typhimurium; radical; DNA damage; YggX homologue.
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Pred. No. 0.004;
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DNA damage;
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RESULT 8 ABB78162

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ggX protein,
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cell, comprises engineering the cell to produce more YggX p;
protein identified from Salmonella enterica Serovar Typhimu;
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YggX homologue.
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radical; DNA damage;
                18-SEP-2001; 2001US-00955502
                                2000US-0234588P
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                                                                        Gralnick JA;
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GRALNICK
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13-JUN-2002
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The specification describes a method for reducing superoxide damage to a cell. The method comprises engineering the cell to produce more than the native amount of YggX protein (a protein identified from Salmonella enterica serovar typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YggX reduces the oxidation of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful for reducing superoxide damage in a bacterial, yeast, mammalian or plant cell. ABB78147-78 represent YggX homologues
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                                                                                              The specification describes a method for reducing superoxide damage t cell. The method comprises engineering the cell to produce more than native amount of YggX protein (a protein identified from Salmonella enterica serovar typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YggX reduces the oxidat of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful freducing superoxide damage in a bacterial, yeast, mammalian or plant cell. ABB78147-78 represent YggX homologues
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Similarity 23.6%;
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GRALNICK J
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radical; D
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cell, comprises engineering the cell to produce more YggX prot
protein identified from Salmonella enterica Serovar Typhimuriu
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                                                                                                                                                                              cell; YggX; Salmonella enterica serovar
DNA damage; YggX homologue.
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               Score 48; DB 5;
Pred. No. 0.004;
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GRALNICK
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The specification describes a method for reducing superoxide damage t cell. The method comprises engineering the cell to produce more than native amount of YggX protein (a protein identified from Salmonella enterica serovar typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YggX reduces the oxidat of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful freducing superoxide damage in a bacterial, yeast, mammalian or plant cell. ABB78147-78 represent YggX homologues
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Pred. No. 0.011;
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Best Local Similarity 23.6%; Pred. No. 0.011;
Matches 13; Conservative 0; Mismatches 42
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The specification describes a method for reducing superoxide damage to a cell. The method comprises engineering the cell to produce more than the native amount of YggX protein (a protein identified from Salmonella enterica serovar typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YggX reduces the oxidation of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful for reducing superoxide damage in a bacterial, yeast, mammalian or plant cell. ABB78147-78 represent YggX homologues
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1 to produce more YggX protein,
enterica Serovar Typhimurium.
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 le damage; cell; YggX;
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GRALNICK J
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plant biocontrol
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Pred. No.
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larity 23.6%;
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hydroxyl radical;
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GRALNICK J A.
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                                                                               Query Match
Best Local Similarity
Matches 13; Conser
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                                            ii proteins and nucleic acids, useful as reagents al disease, as components of antibacterial arrugs, or as biocontrol agents for
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almonella
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                                                                                                                                                                                                                                                            The invention relates to isolated Acinetobacter baumannii nucleic for diagnosing a bacterial disease, as components of antibacterivacines, as targets for antibacterial drugs, to detect the pres A. baumannii and other Acinetobacter species in a sample, in scr compounds for the ability to interfere with the A. baumannii liffor to inhibit A. baumannii infection, and as biocontrol agents for the present sequence represents the amino acid sequence baumannii protein.
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cell, comprises engineering the cell to produce more YggX pl
protein identified from Salmonella enterica Serovar Typhimul
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                                                                                                                                                                                                                                                                                                                                                                                                  11; YggX; Salmonella enterica serovar damage; YggX homologue.
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                                                                                                                                                                                                                       Score 46; DB 6;
Pred. No. 0.012;
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Similarity 23.6%;
13; Conservative
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for diagnosing a bacterial
vaccines, as targets for an
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radical; DNA da
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rendered more resistant to superoxide damage. YggX reduces the oxidation of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful for reducing superoxide damage in a bacterial, yeast, mammalian or plant cell. ABB78147-78 represent YggX homologues
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1 to produce more YggX protein,
enterica Serovar Typhimurium.
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Pred. No. 0.018;
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                                                                                                                                                                                                                                                              Score 45; DB 5;
Pred. No. 0.018;
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DNA damage; }
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                                                                                                                                                                  le damage; cell; YggX; Salmonella enterica serovar typhimurium; radical; DNA damage; YggX homologue.
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Pred. No. 0.018;
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                                   Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium; hydroxyl radical; DNA damage; YggX homologue.
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Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium; hydroxyl radical; DNA damage; YggX homologue.
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The specification describes a method for reducing superoxide damage t cell. The method comprises engineering the cell to produce more than native amount of YggX protein (a protein identified from Salmonella enterica serovar typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YggX reduces the oxidat of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful freducing superoxide damage in a bacterial, yeast, mammalian or plant cell. ABB78147-78 represent YggX homologues
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Pred. No. 0.031;
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30.3%;
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Best Local Similarity 26.8%;
Matches 11; Conservative
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GRALNICK
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almonella
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radical; DNA damage; YggX homologue
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Pred. No. 0.031
0; Mismatches
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DNA damage; Y
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radical; DNA damage;
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cell, comprises engineering the cell to produce more YggX prot
protein identified from Salmonella enterica Serovar Typhimuriu
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hydroxyl radical; DNA damage; YggX homologue
 Mismatches
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11; Conservative
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Reducing superoxide damage to a cell, e.g. bacterial, mammalian or cell, comprises engineering the cell to produce more YggX protein, protein identified from Salmonella enterica Serovar Typhimurium.
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The specification describes a method for reducing superoxide damage to a cell. The method comprises engineering the cell to produce more than the native amount of YggX protein (a protein identified from Salmonella enterica serovar typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YggX reduces the oxidation of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful for reducing superoxide damage in a bacterial, yeast, mammalian or plant cell. ABB78147-78 represent YggX homologues
  plant
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the
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Reducing superoxide damage to a cell, e.g. bacterial, mammalian or cell, comprises engineering the cell to produce more YggX protein, protein identified from Salmonella enterica Serovar Typhimurium.
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Pred. No. 0.43;
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11-JUL-2000;
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NA damage; YggX homologue.
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radical; DNA
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        US2002072118-A1
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Polyhydroxybutyrate synthase; PHB; sphingan; food product; dessert gel;
jelly, jam; beverage; dairy product; gelling agent; rheological modifier;
industrial application.
                                                                                                                                                                                                                                                                                                                                                                    The nucleotide sequence of the PHB operon was obtained from Janes, B. Hollar, J. and Dennis, D. in Dawes, E.A. (ed.) Novel Biodegradable Polymers, Kluwer Academic Publishers, 175-190 (1990). It contains the genes from PHB synthase, 3-ketothiolase and acetoacetyl-CoA reductase. The inventors claim a transgenic plant material contg. foreign DNA encoding a peptide which exhibits 3-ketothilase activity, pref. where to DNA is an open reading from between nucleotides 2696-3877 (phb A gene) 842-2611 (phb C gene) or 3952-4692 (phb B gene) of the Alcaligenes eutrophus PHB operon. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                      Transgenic plants producing poly:hydroxy-alkanoate polymer(s) - transformation with DNA encoding 3-ketothiolase, acetoacetyl-CoA reductase and PHA synthase.
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25-MAR-2003
30-MAY-1993
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 directly
                                                                            Gaps
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beta-ketothiolase; acetoacetyl CoA reductase.
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printed specification, but was obtained in efrom WIPO at ftp.wipo.int/pub/published_pct_
                                                     Score 35; DB Pred. No. 56; Mismatches
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Pred. No. 35;
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larity 35.7%;
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25-MAR-2003
17-APR-1991
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This invention relates to a novel method for the modification of an enzyme participating to the biosynthesis of a poly3-hydroxyalkanoic acid by modifying by recombinant DNA technology. The invention also comprises a gene encoding the above mutant poly3-hydroxybutanoate synthase and a recombinant vector containing the above gene. The method of the invention may be used for the preparation of biodegradable polyesters. The present sequence represents a protein used the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Poly3-hydroxyalkanoic acid; biodegradable polyester; mutant; mutein
                                                   Modification of a biodegradable polyester syr
hydroxybutanoate synthase, its preparation, a
transformant, preparation of a biodegradable
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                                                                                                                              13; Page 116-117; 124pp; Japanese
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N-PSDB; ABX17307.
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                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to mutant strains of Sphingomonas species have a mutation in the gene encoding a protein involved in interstorage polymer polyhydroxybutyrate (PHB) synthesis that allows mutant strains to produce PHB-deficient sphingans. Sphingans are polysaccharides secreted by bacteria of the genus Sphingomonas, invention also relates to a process for preparing clarified sphingoring the taste, texture, stability and appearance of food improving the taste, texture, stability and appearance of food such as dessert gels, confectionery jellies, jams, dairy product beverages, films and coatings. The sphingans are also useful as rheological modifier in industrial applications such as oil-fied drilling and cementitious systems. The present sequence is Alca entrophus polyhydroxybutyrate (PHB) synthase which is used for generation of Sphingomonas elodea phac fragment. phac DNA fragmencodes polyhydroxybutyrate (PHB) synthase protein. (Updated on 2003 to standardise OS field)
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mutation in the gene encoding a protein involved in polyhy
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nthase, a mutant poly3 a recombinant vector,
                                                       ester polymer
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Modification of a biodegradable polyester syr
hydroxybutanoate synthase, its preparation, a
transformant, preparation of a biodegradable
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No.
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This invention relates to a novel method for the modification of an enzyme participating to the biosynthesis of a poly3-hydroxyalkanoic acid by modifying by recombinant DNA technology. The invention also comprises a gene encoding the above mutant poly3-hydroxybutanoate synthase and a recombinant vector containing the above gene. The method of the invention may be used for the preparation of biodegradable polyesters. The present sequence represents a protein used the method of the invention
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N-PSDB; ABX17296.
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Pred. No.
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N-PSDB; ABX17291.
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acid; biodegradable polyester

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This invention relates to a novel method for the modification of an enzyme participating to the biosynthesis of a poly3-hydroxyalkanoic acid by modifying by recombinant DNA technology. The invention also comprises a gene encoding the above mutant poly3-hydroxybutanoate synthase and a recombinant vector containing the above gene. The method of the invention may be used for the preparation of biodegradable polyesters. The present sequence represents a protein used the method of the invention
                                                                                                                                                                                                                                                  Modification of a biodegradable polyester synthase, a mutant poly3. hydroxybutanoate synthase, its preparation, a recombinant vector, transformant, preparation of a biodegradable ester polymer.
                                         Poly3-hydroxybutanoate synthase mutant
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N-PSDB; ABX17278.
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le ester polymer.
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Pred. No. 35;
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Best Local Similarity 42.9%;
Matches 6; Conservative
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N-PSDB; ABX17305.
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Score 34; DB Pred. No. 35; 0; Mismatches
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Conservative
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hydroxybutanoate
N-PSDB; ABX17303
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This invention relates to a novel method for the modification of an enzyme participating to the biosynthesis of a poly3-hydroxyalkanoic acid by modifying by recombinant DNA technology. The invention also comprises a gene encoding the above mutant poly3-hydroxybutanoate synthase and a recombinant vector containing the above gene. The method of the invention may be used for the preparation of biodegradable polyesters. The present sequence represents a protein used the method of the invention
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N-PSDB; ABX17302.
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                                                                                                           This invention relates to a novel method for the modification of an enzyme participating to the biosynthesis of a poly3-hydroxyalkanoic acid by modifying by recombinant DNA technology. The invention also comprises a gene encoding the above mutant poly3-hydroxybutanoate synthase and a recombinant vector containing the above gene. The method of the invention may be used for the preparation of biodegradable polyesters. The present sequence represents a protein used the method of the invention
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         Modification of a biodegradable polyester synthase, a mutan
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transformant, preparation of a biodegradable ester polymer.
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Pred. No. 35;
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Score 34; DB: Pred. No. 35; 0; Mismatches

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This invention relates to a novel method for the modification of an enzyme participating to the biosynthesis of a poly3-hydroxyalkanoic acid by modifying by recombinant DNA technology. The invention also comprises a gene encoding the above mutant poly3-hydroxybutanoate synthase and a recombinant vector containing the above gene. The method of the invention may be used for the preparation of biodegradable polyesters. The present sequence represents a protein used the method of the invention
                                                                                                                                                                                                               Modification of a biodegradable polyester synthase, a mutant hydroxybutanoate synthase, its preparation, a recombinant ve transformant, preparation of a biodegradable ester polymer.
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Best Local Similarity 42.9%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 8; Indels
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                                                   2001JP-00054717.
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                                                                                                                          (RIKA ) RIKAGAKU KENKYUSHO
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N-PSDB; ABX17304.
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                                                  28-FEB-2001;
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5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

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9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

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11: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

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ALIGNMENTS

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RESULT 1
US-09-955-502-20
; Sequence 20, Application US/0995502
; Sequence 20, Application US/0995502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Downs, Diana M.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: 00/234,588
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR APPLICATION NUMBER: 60/234,588
; RIOR APPLICATION NUMBER: 60/234,588
; RIOR APPLICATION NUMBER: 00-09-22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 90
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; ORGANISM: Yersinia pestis
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Sequence 19, Application US/09955502;
Patent No. US20020072118A1;
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to
TITLE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
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US-09-955-502-15
; Sequence 15, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Super; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
. SOFTWARE: Patentin Ver. 2.1
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Sequence 33, Application US/09955502

Patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

APPLICANT: Gralnick, Jeff A.

TITLE OF INVENTION: Method for Preventing Supering Title OF INVENTION: Oxygen-Labile Proteins

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

CURRENT FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: 60/234,588
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Sequence 11, Application US/09955502

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

APPLICANT: Gralnick, Jeff A.

TITLE OF INVENTION: Method for Preventing Superoxide Dam

TITLE OF INVENTION: Oxygen-Labile Proteins

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

CURRENT FILING DATE: 2001-09-18

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 11

LENGTH: 91
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Sequence 12, Application US/09955502

Patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

APPLICANT: Gralnick, Jeff A.

TITLE OF INVENTION: Method for Preventing Superoxide Dam

TITLE OF INVENTION: Oxygen-Labile Proteins

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

CURRENT FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: 60/234,588

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 12

LENGTH: 91
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PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 33
LENGTH: 88
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; ORGANISM: Coxiella burnetii
US-09-955-502-33
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; ORGANISM: Escherichia coli
US-09-955-502-12
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Sequence 13, Application US/09955502

Batent No. US20020072118A1

GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to (TITLE OF INVENTION: Oxygen-Labile Proteins)
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT APPLICATION NUMBER: 60/234,588
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Downs, Diana M.
APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage
TITLE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
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Pred. No. 0.012;
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Pred. No. 0.012
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Patent No. US20020072118A1
GENERAL INFORMATION:
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US-09-955-502-16
; Sequence 16, Application US/09955502
; Patent No. US20020072118A1
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US-09-955-502-14
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| Similarity 23.6%;
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US-09-955-502-18
; Sequence 18, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Grainick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cell;
; TITLE OF INVENTION: Oxygen-Labile Proteins
; TILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR PILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
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| Sequence 17, App. 1...
| Sequence 17, App. 1...
| Sequence 17, App. 1...
| Patent No. US20020072118A1
| GENERAL INFORMATION:
| APPLICANT: Downs, Diana M. APPLICANT: Downs, Jeff A. |
| TITLE OF INVENTION: Method for Preventing Superoxide Damage to TITLE OF INVENTION: Method for Preventing Superoxide Damage to TITLE OF INVENTION: MCYGEN-Labile Proteins
| TITLE OF INVENTION: MCYGEN-Labile Proteins
| FILE REFERENCE: 960296.97559
| CURRENT APPLICATION NUMBER: US/09/955,502
| CURRENT FILING DATE: 2001-09-18
| PRIOR PILING DATE: 2000-09-22
| NUMBER OF SEQ ID NOS: 33
| SOFTWARE: Patentin Ver. 2.1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to
TITLE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 91
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Pred. No. 0.012;
); Mismatches 4
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Pred. No. 0.012;
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Similarity 23.6%;
13; Conservative
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Best Local Similarity 23.6%;
Matches 13; Conservative
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; ORGANISM: Salmonella dublin
US-09-955-502-16
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ORGANISM: Salmonella typhi
-09-955-502-17
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Sequence 21, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
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US-09-955-502-10
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US-09-955-502-21
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US-09-955-502-8
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US-09-955-502-6

i Sequence 6, Application US/09955502

j Patent No. US20020072118A1

j GENERAL INFORMATION:

j APPLICANT: Downs, Diana M.

j APPLICANT: Gralnick, Jeff A.

j TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cellifize Convention: Oxygen-Labile Proteins

j TITLE OF INVENTION: Oxygen-Labile Proteins

j TITLE REFERENCE: 960296.97559

j CURRENT APPLICATION NUMBER: US/09/955,502

j PRIOR APPLICATION NUMBER: 60/234,588

pRIOR FILING DATE: 2000-09-22

j NUMBER OF SEQ ID NOS: 33

j SOFTWARE: PatentIn Ver. 2.1
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Sequence 7, Application US/09955502

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cell:

TITLE OF INVENTION: Oxygen-Labile Proteins

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

CURRENT FILING DATE: 2001-09-18

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.1
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Pred. No. 0.012;
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Pred. No. 0.019;
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US-09-955-502-6
                                                                                                                th Similarity 23.6%;
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                                                              ORGANISM: Salmonella -09-955-502-18
SOFTWARE: Patentin V
SEQ ID NO 18
LENGTH: 91
TYPE: PRT
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Sequence 8, Application US/09955502

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

APPLICANT: Gralnick, Jeff A.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to TITLE OF INVENTION: Oxygen-Labile Proteins

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

CURRENT FILING DATE: 2001-09-18

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 8

LENGTH: 87
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Sequence 10, Application US/09955502

Batent No. US20020072118A1

GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to TITLE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502

CURRENT FILING DATE: 2001-09-18

PRIOR PPLICATION NUMBER: 60/234,588

PRIOR PILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 10

LENGTH: 90
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Pred. No. 0.019;
); Mismatches
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Pred. No. 0.019;
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iilarity 23.6%;
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US-09-955-502-8
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larity 23.6%;
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; LENGTH: 88
; TYPE: PRT
; ORGANISM: Neisseria
US-09-955-502-26
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; Sequence 9, Application US/09955502
; Generat No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cel
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: 60/234,588
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
APPLICANT: Gralnick, Jeff A.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cel

TITLE OF INVENTION: Oxygen-Labile Proteins

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

CURRENT FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: 60/234,588

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 21

LENGTH: 76
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US-09-955-502-26

i Sequence 26, Application US/09955502

j Patent No. US20020072118A1

i GENERAL INFORMATION:

j APPLICANT: Bowns, Diana M.

j APPLICANT: Gralnick, Jeff A.

j TITLE OF INVENTION: Method for Preventing Superoxide Damage to

j TITLE OF INVENTION: Oxygen-Labile Proteins

j FILE REFERENCE: 960296.97559

j CURRENT FILING DATE: 2001-09-18

j PRIOR APPLICATION NUMBER: 60/234,588

j PRIOR FILING DATE: 2000-09-22

j NUMBER OF SEQ ID NOS: 33

j SOFTWARE: PatentIn Ver. 2.1

j SEQ ID NO 26
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Pred. No. 0.027;
0; Mismatches '
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| Similarity 23.6%;
13; Conservative C
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US-09-955-502-21
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13; Conserv
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LENGTH: 88
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-09-955-502-9
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; ORGANISM:
US-09-955-502-
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Sequence 27, Application US/09955502

Patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

APPLICANT: Gralnick, Jeff A.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to (
TITLE OF INVENTION: Oxygen-Labile Proteins

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

CURRENT FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: 60/234,588

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.1

LENGTH: 88

LENGTH: 88

LENGTH: 88
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US-09-955-502-28

Sequence 28, Application US/0995502

Patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to TITLE OF INVENTION: Oxygen-Labile Proteins

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

CURRENT FILING DATE: 2001-09-18

PRIOR PILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 28

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                                            ore 46; DB 9; I ed. No. 0.031; Mismatches 23;
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                                                                                                                      PNELGKRI FENVSQEAWAAWTRHQTMLINENRL
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                                                Score 46;
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US-09-955-502-28
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; ORGANISM: Neisseria meningitidis
US-09-955-502-27
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Best Local Similarity 30.3%;
Matches 10; Conservative
                                               Query Match
Best Local Similarity 30.3%;
Matches 10; Conservative
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RESULT 24
US-09-955-502-29
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                                                                                                                                   SEQ ID NO 24
LENGTH: 87
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US-09-955-502-5
; Sequence 5, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cel:
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR PPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
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                                                                                                           GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to TITLE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
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US-09-955-502-24
; Sequence 24, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to
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red. No. 0.031;
Mismatches 4:
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0.031;
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Pred. No. 0.03:
0; Mismatches
  PNELGKRI FENVSQEAWAAWTRHQTMLI NENRL
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Pred. No.
                                                               3-09-955-502-23
Sequence 23, Application US/09955502
Patent No. US20020072118A1
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US-09-955-502-23
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Similarity 23.6%;
13; Conservative
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ilarity 23.6%;
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TITLE OF INVENTION: Method for Preventing Superoxide Damage to Celling TITLE OF INVENTION: Oxygen-Labile Proteins

TITLE OF INVENTION: Oxygen-Labile Proteins

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

CURRENT FILING DATE: 2001-09-18

PRIOR FILING DATE: 2001-09-22

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 29

LENGTH: 87

TYPE: PRT

ORGANISM: Burkholderia mallei

US-09-955-502-29
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Sequence 30, Application US/0995502

Patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

APPLICANT: Gralnick, Jeff A.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to TITLE OF INVENTION: Oxygen-Labile Proteins

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

CURRENT FILING DATE: 2001-09-18

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 30

LENGTH: 87
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Pred. No. 0.05;
); Mismatches
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TITLE OF INVENTION: Oxygen-Labile Proteins FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
       Proteins
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Pred. No.
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Best Local Similarity 30.3%;
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Similarity 23.6%;
13; Conservative
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; ORGANISM: Pseudomonas putida
US-09-955-502-24
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US-09-955-502-3
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US-09-955-502-31
; Sequence 31, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to;
; TITLE OF INVENTION: Oxygen-Labile Proteins
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
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patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to TITLE OF INVENTION: Oxygen-Labile Proteins

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

CURRENT FILING DATE: 2001-09-18

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.1
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                                           Score 45; DB 9;
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); Mismatches
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Pred. No. 0.05;
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; LENGTH: 87
; TYPE: PRT
; ORGANISM: Thiobacillus ferrooxidans
US-09-955-502-31
; ORGANISM: Burkholderia pseudomallei
US-09-955-502-30
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llarity 22.2%;
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Best Local Similarity 23.6%;
Matches 13; Conservative
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US-09-955-502-32
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LENGTH: 87
TYPE: PRT
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| Sequence 2, Application US/09955502
| Patent No. US20020072118A1
| GENERAL INFORMATION:
| APPLICANT: Downs, Diana M. |
| APPLICANT: Downs, Diana M. |
| APPLICANT: Downs, Diana M. |
| TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and |
| TITLE OF INVENTION: Oxygen-Labile Proteins |
| TITLE OF INVENTION: Oxygen-Labile Proteins |
| FILE REFERENCE: 960296.97559 |
| CURRENT APPLICATION NUMBER: US/09/955,502 |
| CURRENT FILING DATE: 2001-09-18 |
| PRIOR FILING DATE: 2000-09-22 |
| NUMBER OF SEQ ID NOS: 33 |
| SOFTWARE: Patentin Ver. 2.1 |
| SEQ ID NO 2 |
| LENGTH: 87
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Sequence 4, Application US/09955502

Sequence 4, Application US/09955502

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

APPLICANT: Gralnick, Jeff A.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to TITLE OF INVENTION: Oxygen-Labile Proteins

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

CURRENT FILING DATE: 2001-09-18

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 4
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red. No. 0.082;
Mismatches 3
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Pred. No.
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; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica
US-09-955-502-4
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Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
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US-09-955-502-2
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Similarity 26.8%;
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Sequence
FEATURE:
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sequence
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    ; LENGTH: 89
; TYPE: PRT
; ORGANISM: Xylella fastidiosa
US-09-955-502-22
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NAME/KEY: UNSURE
LOCATION: (40)
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NAME/KEY: UNSURE
LOCATION: (24)..(26)
OTHER INFORMATION: c
FEATURE:
NAME/KEY: UNSURE
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LOCATION: (2)
OTHER INFORMATION: C
FEATURE:
NAME/KEY: UNSURE
LOCATION: (4)..(6)
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Best Local Similarity
Matches 8; Conser
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OTHER INFORMATION:
FEATURE:
NAME/KEY: UNSURE
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: (50)
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US-09-955-502-1
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US-09-955-502-25
i Sequence 25, Application US/09955502
j Patent No. US20020072118A1
j Patent No. US20020072118A1
j GENERAL INFORMATION:
i APPLICANT: Gralnick, Jeff A.
i TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cell
i TITLE OF INVENTION: Oxygen-Labile Proteins
i TILE REFERENCE: 960296.97559
i CURRENT APPLICATION NUMBER: US/09/955,502
i CURRENT FILING DATE: 2001-09-18
i PRIOR FILING DATE: 2000-09-22
i NUMBER OF SEQ ID NOS: 33
i SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 32
US-09-955-502-22
iSequence 22, Application US/09955502
iSequence 22, Application:
iSequence 22, Application:
iSequence 22, Application:
iSequence 22, Application:
iSequence 32, Applic
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APPLICANT: Gralnick, Jeff A.

TITLE OF INVENTION: Method for Preventing Superoxide

TITLE OF INVENTION: Oxygen-Labile Proteins

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

CURRENT FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: 60/234,588

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 26.8%; Pred. No. 0.082;
Matches 11; Conservative 0; Mismatches 3
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Best Local Similarity 30.3%; Pred. No. 0.082;
Matches 10; Conservative 0; Mismatches 2
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; TYPE: PRT
; ORGANISM: Bordetella parapertussis
US-09-955-502-3

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US-09-955-502-25
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LENGTH: 87
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APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to
TITLE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 65
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 Length 89;
                               Indels
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ore 44; DB 9;
ed. No. 0.083;
Mismatches
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  Score 44;
Pred. No.
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Patent No. US20020072118A1
GENERAL INFORMATION:
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RESULT 35
US-10-369-493-13068
i Sequence 13068 Application US/10369493
j Publication No. US20030233675A1
j General INFORMATION:
j APPLICANT: Cao, Yongwei
j APPLICANT: Glaman, Barry S.
j TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
j TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
j CURRENT APPLICATION NUMBER: US/0/369,493
j PRIOR APPLICATION NUMBER: US 60/360,039
j PRIOR APPLICATION NUMBER: US 60/360,039
j PRIOR APPLICATION NUMBER: US 60/360,039
j TYPE: PRI
j ORGANISM: Aspergillus nidulans
j PRATURE:
j ORGANISM: Aspergillus nidulans
j PRATURE:
j NAME/KEY: unsure
j NAME/KEY: unsure
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             16;
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           Score 34; DB :
Pred. No. 34;
0; Mismatches
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US-10-369-493-8282
; Sequence 8282, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
    APPLICANT: Cao, Yongwei
    APPLICANT: Hinkle, Gregory J.
    APPLICANT: Slater, Steven C.
    APPLICANT: Chen, Xianfeng
    TITLE OF INVENTION: EXPRESSION OF MICROBIAL
    TITLE OF INVENTION: PLANTS WITH IMPROVED PR
    FILE REFERENCE: 38-10(52052)B
    CURRENT APPLICATION NUMBER: US/10/369,493
    CURRENT FILING DATE: 2003-02-28
    PRIOR FILING DATE: 2002-02-21
    NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 8282
    LENGTH: 391
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; ORGANISM: Thermobifida fusca
US-10-369-493-8282
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               Query Match
Best Local Similarity 42.9%;
Matches 6; Conservative
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; OTHER INFORMATION: unsure
US-10-369-493-13068
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Matches 6; Conser
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/861-3000
TELEFAX: 202/822-0944
TELEFAX: 6714627 CUSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 20005-3518
ZIP: 20005-3518
ZIP: 20005-3518
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/357,521
FILING DATE: 03-Feb-2003
CLASSIFICATION BATA:
APPLICATION NUMBER: US/08/178,257
FILING DATE: 11-JAN-1994
APPLICATION NUMBER: GB 9115245.4
FILING DATE: 16-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N
REGISTRATION NUMBER: 16773
REGISTRATION NUMBER: 16773
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3, N.W.
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US-10-357-521-5
; Sequence 5, Application US/10357521
; Publication No. US20040088751A1
; Publication No. US20040088751A1
; GENERAL INFORMATION:
; APPLICANT: LIEBERGESELL, MATTHIAS
; TITLE OF INVENTION: PRODUCTION OF POLY
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSH
; STREET: 1100 NEW YORK AVENUE, N.1
CITY: WASHINGTON
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ID NO: 5:
                                                     any amino acid
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Pred. No.
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SEQUENCE CHARACTERISTICS:
LENGTH: 356 amino acida
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                           amino
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100.0%; Pi
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US-10-357-521-5
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                                                                                       NAME/KEY: UNSURE
LOCATION: (56)..(62)
OTHER INFORMATION: can be a
FEATURE:
NAME/KEY: UNSURE
LOCATION: (64)..(65)
                                                     can be
                                                                                                                                                                      ; LOCATION: (64)..(65)
; OTHER INFORMATION: can be
US-09-955-502-1
                                                                                                                                                                                                                                                                      Similarity 100
17; Conservative
                                      (54)
FEATURE:
NAME/KEY: UNSURE
LOCATION: (53)..(54)
OTHER INFORMATION:
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Matches 17
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; ORGANISM: Legionella pneumophila
US-10-282-122A-61450
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
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Best Local Similarity 35.3%;
Matches 6; Conservative
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APPLICANT: Wang, Liangsu

APPLICANT: Wang, Liangsu

APPLICANT: Machae, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Trawick, John

APPLICANT: Yamamoto, Robert

APPLICANT: Walling Obres

PRIOR FILING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR PL
       Gaps
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     Indels
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Pred. No. 61;
0; Mismatches
     Mismatches
                                                                                                                                                                                                                                                                                                                                            APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, HIROSHI
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 14669
LENGTH: 393
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US-10-282-122A-61450
; Sequence 61450, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
                                                                                                                                                                                                             ESULT 37
S-10-156-761-14669
Sequence 14669, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-14669
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ilarity 54.5%;
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                                                        42 WXXXQTXLXNE
                                                                                                                    218 WKVAQTTLMNE
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Best Local Similarity
Matches 6; Conser
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APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Kari
APPLICANT: Syskind, Judith
APPLICANT: Syskind, Judith
APPLICANT: Travick, John
APPLICANT: Wammoto, Robert
APPLICANT: Win, H.
TITLE OF INVENTION: Identification of Essential Genes in Microcrganisms
FILE REBERNER: ELITA, 034A
CURBENT PLING DATE: 2003-02-20
PRIOR PELING DATE: 2000-03-20
PRIOR PLING DATE: 2000-03-20
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/203, 335
PRIOR FILING DATE: 2000-10-22
PRIOR APPLICATION NUMBER: 60/257, 931
PRIOR APPLICATION NUMBER: 60/257, 931
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-12-26
PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2000-12-26
PRIOR FILING DATE: 2000-12-26
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-31
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Pred. No. 64;
1; Mismatches
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
SEQ ID NO 5: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 61450
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US-10-282-122A-60959
; Sequence 60959, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
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RESULT 43
US-10-424-599-226079
is Sequence 226079, Application US/10424599
j Publication No. US20040031072A1
j GENERAL INFORMATION:
j APPLICANT: La Roya Thomas J
j APPLICANT: Cao Yongwei
j TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
j TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
j FILE REFERENCE: 38-21(5323)B
j CURRENT FILING DATE: 2003-04-28
j NUMBER OF SEQ ID NOS: 285684
j SEQ ID NO 226079
j LENGTH: 91
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US-10-408-765A-2177

Sequence 2177, Application US/10408765A

Publication No. US20040101874A1

GENERAL INFORMATION:

APPLICANT: Ghosh, Soumitra S.

APPLICANT: Taylor, Steven W.

APPLICANT: Taylor, Steven W.

APPLICANT: Glenn, Gary W.

APPLICANT: Warnock, Dale E.

ITTLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME

FILE REFERENCE: 660088.465

CURRENT APPLICATION NUMBER: US/10/408,765A

CURRENT FILING DATE: 2003-04-04

NUMBER OF SEQ ID NOS: 3077

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2177

LENGTH: 1191
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Pred. No. 1.3e+02;
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Pred. No. 2.4e+02
0; Mismatches
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Pred. No. 53;
0; Mismatches
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ilarity 35.3%;
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  Similarity 23.5%; 4; Conservative
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                                                                    WXXWXXXQTXLXNEXXL
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US-10-408-765A-2177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Glycine max
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Best Local Similarity
Matches 6; Conser
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Best Local Similarity
Matches 5; Conser
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US-10-424-599-276981

Sequence 276981, Application US/10424599

Sequence 276981, Application US/10424599

Sequence 276981, Application US/10424599

Sequence 276981, Application No. US20040031072A1

APPLICANT: La Rosa Thomas J

APPLICANT: Zovalic.David K

APPLICANT: Zovalic.David K

APPLICANT: Zova Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5323)B

CURRENT PILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 276981

LENGTH: 539

TYPE: PRT

ORGANISM: Glycine max
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US-14-59697

US-14-59697
                                                                                                                                        Length 1235;
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Pred. No. 1.5e+02;
2; Mismatches 7;
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Pred. No. 99;
1; Mismatches
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          ; SEQ ID NO 60959
; LENGTH: 1235
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-10-282-122A-60959
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Best Local Similarity 35.7%;
Matches 5; Conservative
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                                                                                                                                       Query Match
Best Local Similarity 30.8%;
Matches 4; Conservative
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WSSWTHLKTSIEN
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ORGANISM: Zea mays
FEATURE:
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Matches
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Query Match

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RESULT 46

US-10-437-963-119949

i Sequence 119949, Application US/10437963

i Sequence 119949, Application US/10437963

i Publication No. US20040123343A1

i Publication No. US20040123343A1

i REPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Vinua

APPLICANT: Cao, Vinua

APPLICANT: Boukharov, Andrey A.

APPLICANT: Bucharov, Andrey A.

APPLICANT: Bucharov, Andrey A.

APPLICANT: Bucharov, Read

APPLICANT: Bucharov, Andrey A.

APPLICANT: Andrew A.

APPLICANT: Andre
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US-10-425-114-53395

Sequence 5335, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Steven

APPLICANT: Steven

APPLICANT: Steven

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21 (53313) B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

LENGTH: 398
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Pred. No. 1.7e+02;
); Mismatches 6;
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Pred. No. 1.6e+02
; Mismatches
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US-10-425-114-64162
; Sequence 64162, Application US/10425114
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ilarity 35.7%;
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Local Similarity 45.5%;
les 5; Conservative
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Matches 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FEATURE:
; OTHER INFORMATION:
US-10-425-114-53395
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ORGANISM: Zea mays
FEATURE:
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Matches 5
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                                                                              Sequence 184047, Application US/10437963
; Sequence 184047, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Fing
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT APPLICATION NUMBER: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 184047
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US-10-437-963-145960

i Sequence 145960, Application US/10437963

j Publication No. US20040123343A1

general Information No. US20040123343A1

general Information No. US20040123343A1

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yongwei

APPLICANT: Shou, Yihua

APPLICANT: Wu, Wei

APPLICANT: Wu, Wei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Brabazuk, Brad

APPLICANT: Brad

APPL
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US-10-437-963-184047
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Pred. No. 1.4e+02); Mismatches (
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larity 35.7%;
Conservative
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38.5%;
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Best Local Similarity
Matches 5; Conserva
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Best Local Similarity
Matches 5; Conser
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US-10-437-963-145960
                          RESULT 44
US-10-437-963-184047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM:
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Sequence 72211, Application US/10425114

Sequence 72211, Application No. US20040034888A1

Publication No. US20040034888A1

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Papaska, Jack E

APPLICANT: Noucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules Acid Molecules

FILE REFERENCE: 38-21(53313)8

FILE REFERENCE: 38-21(53313)8

FILE REFERENCE: 39-31(53313)8

TYPE: PRT

ORGANISM: Zea mays

FRANTURE:

ACID NO 72211

LENGTH: 398

TYPE: PRT

ORGANISM: Zea mays

FRANTURE:

ACID NO 72211

ACID NO 7
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publication No. US2004003488Al

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 64162
LENGTH: 398
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COTHER INFORMATION: Clone ID: LIB3592-097-D6_FLI.pepUS-10-425-114-64162
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Pred. No. 1.7e+02;
); Mismatches 6;
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Pred. No. 1.7e+02
0; Mismatches
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larity 45.5%;
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Best Local Similarity 45.
Lag 5; Conservative
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Best Local Similarity
Matches 5; Conser
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APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 109347
LENGTH: 984
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US-10-437-963-109347
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Pred. No. 3.3e+02;
; Mismatches
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                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
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US-09-955-502-1 139 score: Sequence: Title: Perfect

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

residues 96191526 283366 seqs, Searched: 283366 hits satisfying chosen parameters: Ч Total number

length: 0 length: 2000000000 ន ខេត្ត ភូមិ Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 50 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	nserved hyp	pothetical prot	pothetical prot	unserved hypothe	pothetical prot	pothetical prot	nserved hypothe	unserved hypothe	pothetical prot	nserved hypothe	nserved hypothe	oly (3-hydroxybut	Tothetical prot	pothetical prot	cobable membrane	P-dependent deo	R MSV090 proba	Pothetical prot	[AA1391 protein	AAP-like protein	ate expression	robable membrane	robable soluble	pothetical prot	pothetical prot	hetical pro	onserved hypothe	cetylpolyamine a	ypothetical prot
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ALIGNMENTS

RESULT 1 AI0116 conserved hypothetical protein YPO0953 [imported] - Yersinia pestis (strain CO92) C; Species: Yersinia pestis C; Species: Versinia pestis C; Date: 02-Nov-2001 #sequence revision 02-Nov-2001 #text_change 09-Dec-2002
n, B.W.; Tho Chillingwor K.; Simmond , 2001

A; Title: Genome sequence of Yersinia pestis, the Causalive agent of pragre.
A; Reference number: AB0001; MUID:21470413; PMID:11586360
A; Accession: AI0116
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-90 < KUR>
A; Residues: 1-90 < KUR>
A; Cross-references: GB:AL590842; PIDN:CAC89796.1; PID:g15979022; GSPDB:GN00175
C; Genetics:
A; Gene: YP00953
C; Superfamily: oxygen-labile Fe-S cluster protectant

Gaps ·. Length 90; Indels 42; th Similarity 23.6%; Pred. No. 0.0022; 13; Conservative 0; Mismatches 42 Query Match Best Local S Matches 13

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M.; Co]

RESULT 2
A65082
hypothetical protein b2962 - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Dec-2002
C;Accession: A65082
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
R;Blattner, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: A65082
A;Accession: A65082
A;Accession: A65082
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-91 <BLAT>
A;Cross-references: GB:AE000378; GB:U00096; NID:g1789319; PIDN:AAC75999.1; PID:g1789332, A;Experimental source: strain K-12, substrain MG1655

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T.: Sellers,
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C64013
hypothetical protein H10760 - Haemophilus influenzae (strain Rd KW20)
C; Species: Haemophilus influenzae
C; Date: 18-Aug-1955 #sequence_revision 18-Aug-1995 #text_change 09-Dec-2002
C; Accession: G64013
R; Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kirkness, E.F.; Kerlavage, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Glodek, A.; Kelley, J.M.; Weidman, J.A.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
S; Anthors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter A; Reference number: A64000; MUID:95350630; PMID:7542800
A; Residues: 1-90 <TIGR>
A; Cocssion: C64013
A; Residues: 1-90 <TIGR>
A; Cocss-references: GB:U32760; GB:L42023; NID:g1573764; PIDN:AAC22419.1; PID:g1573769; C; Superfamily: oxygen-labile Fe-S cluster protectant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clayton, R.A.; Kirkness, E.F.; Kerlavage, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.L.; Geoghagen, N.S.M.
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                                                                 hypothetical protein ECs3838 [imported] - Escherichia coli (strain O157:H7, subs C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Dec-2002
C;Accession: F91108
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; H gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. B, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 a;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F91108
A;Accession: F91108
A;Accession: F91108
A;Accession: F91108
A;Cross-references: GB:BA000007; PIDN:BAB37261.1; PID:g13363310; GSPDB:GN00154
A;Cross-references: GB:BA000007; PIDN:BAB37261.1; PID:g13363310; GSPDB:GN00154
A;Cross-references: GB:BA000007; PIDN:BAB37261.1; PID:g13363310; GSPDB:GN00154
A;Genetics:
A;Genetics:
A;Genetics:
C;Genetics:
A;Genetics:
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Pred. No. 0.0057;
0; Mismatches 42;
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ed. No. 0.0035;
Mismatches 4
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Similarity 23.6%;
13; Conservative
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Best Local Similarity 23.6
Matches 13; Conservative
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Matches 13
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K.; Apodaca,
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C; Species: Escherichia coli
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Dec-2002
C; Accession: A85954
R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.
Isler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.;
Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Reference number: DNA
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-91 <STO>
A; Cross-references: GB:AE005174; NID:g12517511; PIDN:AAG58093.1; GSPDB:GN00145; A; Experimental source: strain O157:H7, substrain EDL933
C; Genetics:
A; Gene: yggX
C; Superfamily: oxygen-labile Fe-S cluster protectant
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C; Species: Salmonella enterica subsp. enterica serovar Typhi
A; Note: this species has also been called Salmonella typhi
C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Dec-200
C; Accession: AH0879
R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; Whit, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.
A; Title: Complete genome sequence of a multiple drug resistant Salmonella
A; Reference number: AB0502; MUID:21534947; PMID:11677608
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A; Accession: AH0879
A; Accession: AH0879
A; Accession: AH0879
A; Accession: AH0879
A; Catus: preliminary
A; Molecule type: DNA
A; Residues: 1-91 < PAR>
A; Residues: 1-91 < PAR>
A; Cross-references: GB:AL513382; PIDN:CAD02936.1; PID:g16504189; C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: oxygen-labile Fe-S cluster protectant
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C;Superfamily: oxygen-labile Fe-S cluster protectant
                                                                 Score 48; DB 2;
Pred. No. 0.0035;
0; Mismatches 4:
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Pred. No. 0.0035
0; Mismatches
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13; Conserv
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                                                                                               GSPDB: GN001
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A;Molecule type: DNA
A;Residues: 1-90 <HEI>
A;Residues: 1-90 <HEI>
A;Cross-references: GB:AE004132; GB:AE003852; NID:g9654871; PIDN:AAF93624.1;
A;Experimental source: serogroup OI; strain N1696I; biotype EI Tor
C;Genetics:
A;Gene: VC0451
A;Map position: 1
C;Superfamily: oxygen-labile Fe-S cluster protectant
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C; Species: Buchnera sp.
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change (C; Accession: E84994
R; Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, Nature 407, 81-86, 2000
A; Title: Genome sequence of the endocellular bacterial symbiont cA; Reference number: A84930, MUID: 20445173; PMID: 10993077
A; Accession: E84994
A; Status: preliminary
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33.1%; Score 46; DB 2; Length 88;
Best Local Similarity 30.3%; Pred. No. 0.009;
Matches 10; Conservative 0; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                Length 90;
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Pred. No. 0.0057;
0; Mismatches 4
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0
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Similarity 23.6%;
13; Conservative (
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Best Local S
Matches 13
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conserved hypothetical protein PAS148 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Dec-2002 C;Accession: H83003 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathog A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathog A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathog A;Accession: H83003 A;Accession: H8303 A;Accession: H83003 A;Accession: Assidues: 1-90 csroo A;Accession: H8300 csroo A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Gene: PA5148 C;Superfamily: oxygen-labile Fe-S cluster protectant
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C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Date: 1B-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Dec-2002
C;Accession: C82624
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MuID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: C82624
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: C82624
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.; Miyaki, C.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Pred. No. 0.0094;
0; Mismatches 42;
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Pred. No. 0.024;
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A; Molecule type: DNA
A; Residues: 1-93 <STO>
A; Cross-references: GB: AP000398; GS
A; Experimental source: strain APS
C; Genetics:
A; Gene: yggX; BU553
C; Superfamily: oxygen-labile Fe-S c
                                                                                                                                                                                                                                                                                          th similarity 23.6%; 13; Conservative
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Best Local Similarity 30.3%;
Matches 10; Conservative
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GSPDB:GN001

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401 WQAWHDTLTRLYNRGAL
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Best Local S
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F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.P. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A, Authors: da Silva, A.C.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; ZA; Contents: annotation C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: oxygen-labile Fe-S cluster protectant
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F90965
hypothetical protein ECs2694 [imported] - Escherichia coli (strain O157:H7, sult; Species: Escherichia coli
C; Species: Escherichia coli
C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C; Accession: F90965
R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Accession: F90965
A; Anolecule type: DNA
A; Residues: 1-564 < HAX>
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R; Pecoples, O.P.; Sinskey, A.J.
J; Biol. Chem. 264, 15298-15303, 1989

A; Title: Poly-beta-hydroxybutyrate (PHB) biosynthesis in Alcaligenes eutrophus preliminary
A; Reference number: A34341; MUID:89359357; PMID:2670936

A; Residues: 1.589 < PEO>
A; Residues: 1.589 < PEO>
A; Residues: 1.589 < PEO>
A; Residues: 1.580 < PEO>
A; Accession: A34341; MUID:9141958; PIDN:AAA21975.1; PID:g141959
A; Coos-references: GB:055003; NID:g141958; PIDN:AAA21975.1; PID:g141959
A; Experimental source: strain H16
B; Schubert, P.; Krueger, N.; Steinbuechel, A.
J; Title: Molecular analysis of the Alcaligenes eutrophus poly(3-hydroxyburomoter.
A; Reference number: A39190; MUID:91100279; PMID:1987116
A; Ctoos-references: GB:MG-3441; NID:g141964; PIDN:AAA21979.1; PID:g141965
A; Note: the authors translated the codon TAC for residue 120 as Thr C; Superfamily: poly(3-hydroxyalkanoic acid) synthase phbC
C; Keywords: acyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 0.028
0; Mismatches
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                                                                                                                                                                                                                                  31.7%;
Similarity 47.1%;
8; Conservative
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ilarity 42.9%;
Conservative
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hypothetical protein 23047 [imported] - Escherichia coli (strain O157:H7, substrain EDL93: C; Species: Escherichia coli C; Species: Escherichia coli C; Species: Escherichia coli C; Species: Escherichia coli C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C; Accession: F85813
R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Residues: 1-564 <STO>
A; Residues: 1-564 <STO>
A; Crossines: Treferences: GB:AE005174; NID:g12516062; PIDN:AAG56970.1; GSPDB:GN00145; UWGP:2304 A; Experimental source: strain O157:H7, substrain EDL933
C; Genetics:
A; Genetics:
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A; Cross-references: GB:AE000287; GB:U00096; NID:g1788257; PIDN:AAC75 A; Experimental source: strain K-12, substrain MG1655 C; Genetics:
A; Start codon: TTG
C; Keywords: transmembrane protein F;363-46/Domain: transmembrane #status predicted <TM1>
F;363-46/Domain: transmembrane #status predicted <TM2>
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A;Cross-references: GB:BA000007; PIDN:BAB36117.1; PID:g13362162; A;Experimental source: strain O157:H7, substrain RIMD 0509952 C;Genetics: A;Gene: ECs2694
                                                                                                                                        564;
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Pred. No. 26;
0; Mismatches
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Pred. No. 26;
0; Mismatches
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Best Local Similarity 35.3%;
Matches 6; Conservative
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Matches 6; Conservative
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KIAALS'S process (Man)
C'Species: Homo sapiens (Man)
C'Species: Homo sapiens (Man)
C'Species: Homo sapiens (Man)
C'Sate: 30.0un-2002 #sequence_revision 03-Jun-2002 #text_change 23-Sep-2002
C'Accession: C59436; D59436
R'Sydagase, T, Kikuno, R.; Ishikawa, K.I.; Hirosawa, M.; Ohara, O.
DNA Res. 7, 65-73, 2000
A;Title: Prediction of the coding sequences of unidentified human genes. XVI. The complet
A;Reference number: C59436
A;Actession: C59436
A;Actus: preliminary
A;Molecule type: mRNA
A;Residues: 1-1194 <NAGA
A;Residues: 1-1194 <NAGA
A;Reference number: D59436
A;Actus: preliminary
A;Actus: preliminary
A;Actus: preliminary
A;Actus: preliminary
A;Molecule type: mRNA
A;Residues: 1-1194 <OHA>
A;Cross-references: GB:BAA92629; PID:g7243163; PIDN:BAA92629.1
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                                                                                                                                                                            NID:g1652725; PIDN:BAA17660.1; to the EMBL Data Library, June
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C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-1
C;Accession: T38084
R;Gentles, S.; Odell, C.; Churcher, C.M.; Barrell, B.G.; Rajandream submitted to the EMBL Data Library, November 1995
A;Reference number: 221768
A;Reference number: 221768
A;Reference number: 221768
A;Reference number: 221768
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-3655 <GEN>
A;Residues: 1-3655 <GEN>
A;Residues: 1-3655 <GEN>
A;Cross-references: EMBL: Z68136; PIDN: CAA92239.1; GSPDB: GN00066; SPI
A;Experimental source: strain 972h-; cosmid c1F5
C;Genetics:
A;Gene: SPDB:SPAC1F5.11c
A;Introns: 22/1
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Pred. No. 32;
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N
A;Reference number: S74322; MUID:97061201; PMID:
A;Accession: S77102
A;Status: nucleic acid sequence not shown; trans
A;Molecule type: DNA
A;Residues: 1-420 <KAN>
A;Cross-references: EMBL:D90908; GB:AB001339; NI
A;Note: the nucleotide sequence was submitted to
C;Genetics:
A;Start codon: GTG
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ilarity 38.5%;
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C59436
KIAA1391 protein [imported]
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Best Local Similarity
Matches 5; Conser
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Matches 5; Conser
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                                                                                            ATP-dependent decoxyribonuclease (chain A) homolog lmo2267 [imported] - Listeria monocyted (Species: Listeria monocytogenes (Species: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 (Species: 2001 November: November:
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S77102
hypothetical protein slr1865 - Synechocystis sp. (strain PCC 6803)
C; Species: Synechocystis sp.
A; Variety: PCC 6803
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C; Accession: S77102
R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis s.
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C;Accession: T28251
R;Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D J. Virol. 73, 533-552, 1999
A;Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A;Reference number: Z20484; MUID:99102612; PMID:9847359
A;Accession: T28251
A;Accession: T28251
A;Accession: T28251
A;Accession: T28251
A;Accession: T28251
A;Cross-references: EMBL:AF063866; NID:g4049647; PIDN:AAC97640.1; PIC;Genetics:
A;Note: MSV090
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Pred. No. 53;
2; Mismatches
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llarity 30.8%;
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, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, Science 269, 496-512, 1995
A; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; A; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae A; Reference number: A64000; MUID:95350630; PMID:7542800
A; Reference number: A64000; MUID:95350630; PMID:7542800
A; Accession: C64097
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-593 <TIGR>
A; Cross-references: GB:U32765; GB:L42023; NID:g1573838; PIDN:AAC22487.1; PID:g1C; Superfamily: soluble lytic transglycosylase
C; Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                       Score 31; DB Pred. No. 71; 0; Mismatches
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Best Local Similarity 35.3%;
Matches 6; Conservative
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larity 28.6%;
Conservative
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Matches 4
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AC0754
probable membrane protein STY2194 [imported] - Salmonella enterica subsp. enterica serovar Typhi
C; Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AC0754
R;Packhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; Wain, J.; Churcher, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Residues: 1-567 <PAR>A;Residues: 1-567 <PAR>A;Gross-references: GB:AL513382; PIDN:CAD05734.1; PID:g16503227; GSPDB:GN00176
C;Genetics:
A;Gene: STY2194
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ley, J.M.; Weidman
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                                                                                                                                                                                                                                  virus
                                                                                                                                                                 RESULT 21
T10392
late expression factor 7 protein - Orgyia pseudotsugata nuclear polyhedrosis virus, OpMNPV
C; Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpMNPV
C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C; Accession: T10392
R; Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.
Virology 229, 381-399, 1997
A; Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyh A; Reference number: Z17011; MUID:97271300; PMID:9126251
A; Reference number: Z17011; MUID:97271300; PMID:9126251
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-211 <AHR>
A; Residues: 1-211 <AHR>
C; Superfamily: Orgyia pseudotsugata nuclear polyhedrosis virus late expression fa
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C64097
probable soluble lytic transglycosylase (EC 3.2.1.-) - Haemophilus i probable soluble lytic transglycosylase (EC 3.2.1.-) - Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 22-C;Accession: C64097
C;Accession: C64097
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kell
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2; Mismatches 7; Inde
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     Pred. No. 2.3e+02
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Pred. No. 68;
0; Mismatches
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Similarity 54.5%; 6; Conservative
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illarity 35.3%;
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larity 35.7%;
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Best Local Similarity
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K.; Apodaca,
                                                                                                                                                                                                                             substrain
                                                                                                                                                         RESULT 24
F91126
hypothetical protein EC83982 [imported] - Escherichia coli (strain O157:H7, substrail C;Species: Escherichia coli
C;Species: Escherichia coli
C;Species: Escherichia coli
C;Accession: F91126
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and A;Recession: F91126
A;Recession: F91126
A;Accession: P91126
A;Accession: preliminary
A;Accession: preliminary
A;Cross-references: GB:BA000007; PIDN:BAB37405.1; PID:g13363455; GSPDB:GN00154
A;Genetics:
A;Genetics:
A;Genetics:
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 Gaps
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R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Pota Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:: A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-99 <STO>
A;Cross-references: GB:AE005174; NID:g12517690; PIDN:AAG58233.1; GSPIC;Genetics:
A;Genetics:
A;Genetics:
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Mismatches
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Length

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hypothetical protein [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (Mouse-ear Cress) (C. Species: Association (C. Mar-2001) (C. Mar-2001) (C. Mar-2001) (C. Mar-2001) (C. Mar-2001) (C. M. E. Crear) (C. M. E. Conn, C. M. Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C. M.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., ansen, N.F.; Hughes, B.; Huizar, L. Mature 408, 816-820, 2000 (A.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Mu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. (A. M.; Sun, H.; Tallon, I. A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A; Accession: A86127 (A. Molecule type: DNA)
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct;
A; Reference number: A69000; MUID: 98037514; PMID: 9371463
A; Reference number: A69000; MUID: 98037514; PMID: 9371463
A; Reference number: A69000; MUID: 98037514; PMID: 9371463
A; Residues: C69026
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-331 <MTH>
A; Residues: 1-331 <MTH>
A; Experimental source: strain Delta H
C; Genetics:
A; Coss-references: Strain Delta H
C; Genetics:
A; Genetics:
A; Coss-references: Strain Delta H
C; Genetics:
A; Coss-references: Strain Delta H
C; Genetics:
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C; Coss-references: Strain Delta H

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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 04-Ma C;Accession: T04525
R;Bevan, M.; Brandt, P.; Dose, S.; Jarke, D.; Scharfe, M.; Schon, O.; Submitted to the Protein Sequence Database, February 1999
A;Reference number: Z15376
A;Accession: T04525
A;Accession: T04525
A;Residues: 1-331 <BEV>
A;Residues: 1-331 <BEV>
A;Cross-references: EMBL:AL035353
A;Experimental source: cultivar Columbia; BAC clone F16A16
C;Genetics:
A;Map position: 4
A;Introns: 76/2; 269/2; 286/2
A;Note: F16A16.150
C;Superfamily: Arabidopsis thaliana hypothetical protein F16A16.150
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5; Conservative
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5; Conserv
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Gibson, R.; Jiwani,
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C69026
acetylpolyamine aminohydrolase - Methanobacterium thermoautotrophicum (strain Delta C; Species: Methanobacterium thermoautotrophicum
C; Species: Methanobacterium thermoautotrophicum
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C; Accession: C69026
C; Accession: C69026
R; Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, ; Smith, D.R.; Doucette-Stamm, L.A.; Mang, Y.; Wierzbowski, J.; Gibson, R.; Jiwan; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwan;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conserved hypothetical protein STY3411 [imported] - Salmonella enter C; Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-N. C;Accession: AE0895 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L., S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelta A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelta A;Authors: Preliminary A;Reference number: AB0502; MUID:21534947; PMID:11677608 A;Accession: AE0895 A;Eatus: Dreliminary A;Molecule type: DNA A;Residues: 1-99 cPAR> A;Cross-references: GB:AL513382; PIDN:CAD07755.1; PID:g16504306; GSPI C;Genetics: A;Gene: STY3411
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A;Molecule type: DNA
A;Residues: 1-99 <BLAT>
A;Cross-references: GB:AE000392; GB:U00096; NID:g2367194; PIDN:AA
A;Experimental source: strain K-12, substrain MG1655
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                                                                                                                                                                                                                                                                                        hypothetical protein b3100 - Escherichia coli (strain K-12) C; Species: Escherichia coli C; Species: Escherichia coli C; Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change C; Accession: A65099 R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Science 277, 1453-1462, 1997 Science 277, 1453-1462, 1997 A; Title: The complete genome sequence of Escherichia coli K-12 A; Reference number: A64720; MUID: 97426617; PMID: 9278503
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Pred. No. 22;
2; Mismatches
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28.6%;
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                     Conservative
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C.; Hamlin, D.; Gordon; Hamlin, N.; Holroyd, S.; Squares, S.

22-Oct-1999

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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go conor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Residues: C70606
A;Residues: 1-711 <COL>
A;Residues: 1-711 <COL>
A;Residues: 1-711 <COL>
A;Experimental source: strain H37Rv
C;Genetics:
A;Genetics:
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B75573
Conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: B75573
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dc, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalt S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein W01A11.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Saccession: T29644
R;Blanchard, M.; Bradshaw, H.
Submitted to the EMBL Data Library, July 1996
A;Description: The sequence of C. elegans cosmid W01A11.
A;Reference number: Z20658
A;Refe
                                                                      RESULT 33
C70606
probable fadE34 protein - Mycobacterium tuberculosis (strain H37RV)
C; Species: Mycobacterium tuberculosis
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-
C; Accession: C70606
R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.;
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Pred. No. 1.4e+02;
; Mismatches 5;
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L; Mismatches 8;
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larity 45.5%;
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Best Local Similarity
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C;Species: Gallus gallus (chicken)
C;Dete: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
C;Dete: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
C;Dete: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
C;Dete: 30-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
C;Dete: 30-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
C;Dete: 30-Mar-1998
R;Dounder: 300386
A;Title: 1dentification in chickens of an evolutionarily conserved cellular ets-2 gene
A;Reference number: $00386; MuID:88283637; PMID:329399
A;Reference number: $00386; MuID:88283637; PMID:3293999
A;Reference number: $00386
A;Moles: 1-479 & ENGUS
A;Residues: 1-479 & ENGUS
A;Residues: 1-479 & ENGUS
A;Residues: 1-479 & ENGUS
A;Residues: 1-479 & ENGUS
C;Reywords: DNA binding; nucleus; phosphoprotein; proto-oncogene; transcription factor; F;34-167/Region: helix-loop-helix #status preddicted
F;34-457/Region: helix-loop-helix #status preddicted
F;375-453/Domain: ets DNA-binding domain homology <ETS>
F;415-421/Region: nuclear location signal
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                                           PDB:GN00141
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A; Reference number: Z21837
A; Accession: T39230
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-418 < CHU>
A; Residues: 1-418 < CHU>
A; Experimental source: strain 972h-; cosmid c9G1
C; Genetics:
A; Genetics:
A; Genetics:
A; Map position: 1
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Pred. No. 84;
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1; Mismatches
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Pred. No. 95;
1; Mismatches
                                   GB:AE005172; NID:93482913;
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A;Residues: 1-385 <S;
A;Cross-references: (
C;Genetics:
A;Map position: 1
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CORECAL division inhibitor sull - Escherichia coli (strain K-12)

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cell division inhibitor sulA - Salmonella typhimurium
C;Species: Salmonella typhimurium
C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #te
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Yamada, M.; Yasuda
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R; Dairi, T.; Hamano, Y.; Igarashi, Y.; Furumai, T.; Oki, T. Biosci. Biotechnol. Biochem. 61, 1445-1453, 1997
A; Title: Cloning and nucleotide sequence of the putative polyketide A; Reference number: JC5850; MUID: 97480928; PMID: 9339544
A; Molecule type: DNA
A; Residues: 1-153 < DAI>A; Cross-references: DDBJ: DB7924
C; Comment: This enzyme catalyzes repeated condensation cycles of acy C; Genetics:
A; Genetics:
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euchi, C.; Wada, T.; Watanabe,
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A; Title: Genome sequence of the radioresistant bacterium Dei A; Reference number: A75250; MUID:20036896; PMID:10567266
A; Accession: B75573
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-546 <WHI>
A; Residues: 1-546 <WHI>
A; Cross-references: GB:AE001863; GB:AE001825; NID:g6460670; A; Experimental source: strain R1
C; Genetics:
A; Genetics:
A; Genetics:
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                                                                                                                                    GB:AE001825; NID:g6460670;
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C; Date: 25-Apr-1997 #sequence_revision 25-Ap. C; Accession: S76185
R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C. DNA Res. 3, 109-136, 1996
A; Title: Sequence analysis of the genome of
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-124 < KAN>
A; Cross-references: EMBL: D90914;
A; Note: the nucleotide sequence w
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R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoy, gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinag, DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia col. A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: B90759
A;Accession: B90759
A;Molecule type: DNA
A;Residues: 1-169 <HAY>
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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R; Freudl, R.; Braun, G.; Honore, N.; Cole, S.T.
Gene 52, 31-40, 1987
A; Title: Evolution of the enterobacterial sulA gene: a component
A; Reference number: A29016; MUID:87248093; PMID:3297925
A; Accession: B29016
A; Molecule type: DNA
A; Residues: 1-169 <FRE>
A; Cross-references: GB:M16324; NID:g154377; PIDN:AAA27230.1; PID
C; Genetics:
A; Genetics:
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A; Genetics:
A; Genetics:
C; Function:
A; Description: inducible cell division inhibitor
A; Note: expression of sulA is repressed by lexA protein
C; Superfamily: cell division inhibitor sulA
C; Keywords: cell division control; SOS response
                                                   component
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Call division inhibitor sulA - Enterobacter aerogenes

C; Species: Enterobacter aerogenes

C; Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change

C; Accession: C29016

R; Freudl, R.; Braun, G.; Honore, N.; Cole, S.T.

Gene 52, 31-40, 1987

A; Title: Evolution of the enterobacterial sulA gene: a component

A; Reference number: A29016; MUID:87248093; PMID:3297925

A; Residues: 1-169 <FRE>

A; Accession: C29016

A; Molecule type: DNA

A; Residues: 1-169 <FRE>

A; Cross-references: GB:M16467; NID:g148376; PIDN:AAA24810.1; PID

C; Genetics:

A; Gene: sulA

C; Function: inducible cell division inhibitor

A; Note: expression of sulA is repressed by lexA protein

C; Superfamily: cell division inhibitor sulA

C; Superfamily: cell division inhibitor sulA

C; Keywords: cell division control; SOS response
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hypotherical protein sulA [imported] - Escherichia coli (strain O157:H7, substrain EDL93: C; Species: Escherichia coli C; Species: Escherichia coli C; Date: 16-Feb-2001 #text_change 14-Sep-2001 C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C; Accession: H85622 R; Perna, T: Plunkett III, G; Burland, V; Mau, B; Glasner, J.D; Rose, D.J.; Mayhew, ijler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001 A; Tile: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551 A; Reference number: A85480; MUID:21074935; PMID:11206551 A; Residues: 1-169 <STO>A; Cross-references: GB:AE005174; NID:g12514143; PIDN:AAGS5444.1; GSPDB:GN00145; UWGP:Z13(A; Experimental source: strain O157:H7, substrain EDL933 C; Genetics: A; Genetics: A
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Salmonella enterica serova
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, L.; White,
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AB0627
cell division inhibitor [imported] - Salmonella enterica subsp. entic; Species: Salmonella enterica subsp. enterica serovar Typhi
C; Species: Salmonella enterica subsp. enterica serovar Typhi
C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-1
C; Accession: AB0627
R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D. th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L., S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skell A; Reference number: AB0502; MUID:21534947; PMID:11677608
A; Reference number: AB0502; MUID:21534947; PMID:11677608
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-169 < PAR>
A; Residues: 1-169 < PAR>
A; Cross-references: GB:AL513382; PIDN:CAD08197.1; PID:g16502246; GS: C; Genetics:
A; Gene: STY1092
C; Superfamily: cell division inhibitor sulA
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Davis, P.; Davies, R.M.; Dowd,
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                                                               Score 29; DB
Pred. No. 59;
0; Mismatches
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Pred. No. 59;
0; Mismatches
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Pred. No. 59;
0; Mismatches
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sulA
cell division inhibitor
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ilarity 35.7%;
Conservative
                                                               20.9%;
Similarity 35.7%;
5; Conservative
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5; Conservative
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CESP: F19C7

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M.; Gordon-Kamm,
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R;Wood, D. W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Expo, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; M.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordonster, E.W.

A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Residues: 1-425 < KUR>
A;Residues: 1-425 < KUR>
A;Residues: 1-425 < KUR>
A;Genetices: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Map position: circular chromosome
                                                                                                                                                                                                                                                          PIDN: AAA83507.1;
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                                        Kibe, T.
submitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid F19C7.
A;Reference number: Z18461
A;Accession: T16103
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-310 < LET>
A;Coss-references: EMBL: U42439; NID: g1123106; PID: g1123109; PID
C;Genetics:
A;Gene: CESP: F19C7.3
A;Introns: 71/2; 178/3; 269/2
C;Superfamily: Caenorhabditis elegans hypothetical protein C24H1
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C; Species: rice dwarf virus
C; Date: 09-Aug-1995 #sequence_revision 19-Oct-1995 #te
C; Accession: JC1069
R; Chu, R.Y.; Zhang, X.; Pan, N.S.; Chen, Z.L.
Acta Bot. Sin. 35, 115-120, 1993
A; Title: The cDNA cloning and nucleotide sequence of t
A; Reference number: JC1069
A; Accession: JC1069
A; Molecule type: mRNA
A; Residues: 1-372 < CHU>
C; Genetics:
A; Map position: segment 10
C; Superfamily: wound tumor virus nonstructural proteir
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Pred. No. 1e+02;
); Mismatches
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Best Local Similarity 23.5%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 38.5%;
Matches 5; Conservative
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T16103
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Cob(1) alamin adenosyltransferase - Deinococcus radiodurans
Cobcies: Deinococcus radiodurans
Cobcies: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2003
Cobcies: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2003
Cobciesion: H75618
Robert Dec-1999 #sequence of the radioresistant bacterium Deinococcus radiodurans Robert 1571-1577, 1999
Accession: H75618
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L.; White,
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                                                                                                                      eubsp.
                                                                                                   probable membrane protein STY2766 [imported] - Salmonella enterica subspreade serovar Typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-No
C;Accession: AH0821
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.;
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.;
, S.; Moule, S.; O'Gazoa, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelto
A;Title: Complete genome sequence of a multiple drug resistant Salmon
A;Accession: AH0821
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: GB:AL513382; PIDN:CAD02724.1; PID:g16503736; GSPD
C;Genetics:
A;Gene: STY2766
C;Superfamily: hypothetical protein H10370
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C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change
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A;Cross-references: GB:AE001826; NID:g6460827; PIDN:AAF12570.1; A;Experimental source: strain R1
C;Genetics:
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A;Map position: megaplasmid
A;Genome: plasmid
A;Note: plasmid MP1
C;Superfamily: ATP:cob(I)alamin adenosyltransferase,
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Pred. No. 71;
1; Mismatches
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Pred. No. 71;
0; Mismatches
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nilarity 29.4%;
Conservative
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Best Local Similarity 44.4%;
Matches 4; Conservative
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Matches 5; Conserva
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C58

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Synochopyruvate hydratase (EC 4.2.1.11) - Synechocystis sp. (strain PCC 6803)

N,Alternate names: protein s1r0752

C;Species: Synechocystis sp.
A;Variety: PCC 6803

C;Accession: S76837

C;Accession: S76837

R;Kaneko, T: Sarb. So; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O; K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
A;Reference number: S74322; MUID:97061201; PMID:8905231

A;Refatus: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-432 cKAN>
A;Residues: 1-432 cKAN>
A;Rote: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: enolase
C;Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase
                                                                                                                                                                                                                                                      hypothetical protein AGR_C_3154 [imported] - Agrobacterium tumefaciens (strain C58, Cere C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Date: 30-Sep-2001 #text_change 18-Nov-2002
C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C; Date: 30-Sep-2001
R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A; Reference number: A97359; MUID:21608551; PMID:11743194
A; Reference number: A97359; MUID:21608551; PMID:11743194
A; Residues: Propeinminary
A; Molecule type: DNA
A; Residues: 1-429 < KUR>A; Molecule type: DNA
A; Residues: 1-429 < KUR>A; Cross-references: GB:AE007869; PIDN:AAK87490.1; PID:g15156815; GSPDB:GN00169
C; Genetics:
A; Map position: circular chromosome
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ppas, C.; Markelz, B.;
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SwissProt_42:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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C STRAIN=KIMS / Biovar Mediaevalis;

C STRAIN=KIMS / Biovar Mediaevalis;

X MEDLINE=22137863; PubMed=12142430;

X Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,

X Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,

X Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,

X Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,

X Perry R.D.;

"Genome sequence of Yersinia pestis KIM.";

"Genome sequence of Yersinia pestis KIM.";
                                                                                D Y953 YERPE STANDARD; ...,

C Q8ZHE7;

T 10-OCT-2003 (Rel. 42, Last sequence update)

T 10-OCT-2003 (Rel. 42, Last sequence update)

T 10-OCT-2003 (Rel. 42, Last annotation update)

Hypothetical UPF0269 protein YP00953/Y3340.

N YP00953 OR Y3340.

S Yersinia pestis.

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

C Enterobacteriaceae; Yersinia.

NCBI_TaxID=632;
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SEQUENCE FROM N.A.
STRAIN=CO-92 / Biovar Orientalis;
MEDLINE=21470413; PubMed=11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Chillingworth T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Feltwell T., Hamlin N., Holroyd S., Jagels K., Rarlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Genome sequence of Yersinia pestis, the causative agent of plague.";
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EMBL; AE013935; AAM86890.1;
HAMAP; MF_00686; -; 1.
InterPro; IPR007457; DUF495.
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-!- SIMILARITY: Belongs to the UPF0269 family.

-!- SIMILARITY: Belongs to the UPF0269 family.

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STRAIN=Nine Mile phase I / RSA 493;

MEDLINE=22608657; PubMed=12704232;

Seshadri R., Paulsen I.T., Eisen J.A., Read T.D., Nelson K.E., Nelson W.C., Ward N.L., Tettelin H., Davidsen T.M., Beanan M.J. DeBoy R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R. Khouri H.M., Lee K.H., Carty H.A., Scanlan D., Heinzen R.A., Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F., "Complete genome sequence of the Q-fever pathogen, Coxiella brocketii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MTRRIICOKLGKEADALNYSPYPGELGERIYNHISEQAWQAWLSHQTMLINEY
                                                                                                  Coxiella burnetii.
Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
Coxiellaceae; Coxiella.
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 Pfam; PF04362; DUF495; 1.
PIRSF; PIRSF029827; DUF495; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 90 AA; 10707 MW; C7374E6855653F65 CRC64;
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Pred. No. 0.0007;
); Mismatches 42;
                                                     th 35.3%; Score 49; DB 1; 1 Similarity 23.6%; Pred. No. 0.00042; 13; Conservative 0; Mismatches 42;
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical UPF0269 protein CBU0941.
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(Rel. 42, Last sequence update)
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InterPro; IPR007457; DUF495.
Pfam; PF04362; DUF495; 1.
PIRSF; PIRSF029827; DUF495; 1.
Hypothetical protein; Complete p.
SEQUENCE 90 AA; 10482 MW; 70
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                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=306 / ATCC 13902 / XV 101;

MEDLINE=22022145; PubMed=12024217;

A Silva A.C.R. Ferraro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

A Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

Alves L.M.C., do Amaral A.M., Estolini M.C., Camargo L.E.A.,

Alves L.M.C., do Amaral A.M., Cardozo J., Chambergo F., Ciapina L.P.,

A Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

Faria J.B., Ferreira A.J.S., Ferreira R.C., Gruber A.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins E.C., Machado M.A., Manceira A.M.B.N., Martinez-Rossi N.M.,

Mortins E.C., Maidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

Martins E.C., Maidanis J., Nenck C.F.M., Miyaki C.Y., Coliveira V.R.,

Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

"Comparison of the genomes of two Xanthomonas pathogens with differing hot specificities.",

Nature 417:459-463(2002).

LI SIMILARITY: Belongs to the UPF0269 family.
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STRAIN=E1 Tor N16961 / Serotype O1
MEDLINE=20406833; PubMed=10952301;
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HAMAP; MF_00686; -; 1.
InterPro; IPR007457; DUF495.
Pfam; PF04362; DUF495; 1.
PIRSF; PIRSF029827; DUF495; 1.
Hypothetical protein; Complete presents of AA; 10492 MW; B2
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                                                                                              Xanthomonas axonopodis (pv. ci
Bacteria; Proteobacteria; Gamm
Xanthomonadaceae; Xanthomonas.
NCBI_TaxID=92829;
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Similarity 23.6%;
13; Conservative
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Electrophoresis
-!- SIMILARITY:
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White O.,
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    nn M.L.,
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STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=95350630; PubMed=7542800;

METALINE B.D., Merrick J.D., Merrick J.D., Merrick J.M.,

Meidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Meidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Meidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Meidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Meidman J.F., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

Menter J.C.,

Mente
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the cholera pathogen V
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Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwi
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Ve
Fraser C.M.;
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972331B2600B3184
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Pred. No. 0.0012;
0; Mismatches 4:
                                                                                                                                                                                                                                                           family
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01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
HI0760.
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MEDLINE=20137488; PubMed=10675023;
Langen H., Takacs B., Evers S., Berndt Gray C., Fountoulakis M.;
"Two-dimensional map of the proteome of
                                                                                                                                                                                                       cholerae.";
Nature 406:477-483(2000).
-!- SIMILARITY: Belongs to the UPF0269
                                                                                                                                                                                 both chromosomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE004132; AAF93624.1; -.
TIGR; VC0451; -.
HAMAP; MF_00686; -; 1.
InterPro; IPR007457; DUF495.
Pfam; PF04362; DUF495; 1.
PIRSF; PIRSF029827; DUF495; 1.
HYPOthetical protein; Complete p.
SEQUENCE 90 AA; 10647 MW; 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemophilus influenzae.
Bacteria; Proteobacteria; Gan
Pasteurellaceae; Haemophilus.
NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity 23.6%;
13; Conservative
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Science 269:496-512(1995)
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Best Local S
Matches 13
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales
Pasteurellaceae; Pasteurella.
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STRAIN=Pm70;
MEDLINE=21145866; PubMed=11248100;
May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kander Genomic sequence of Pasteurella multocida Pm70."; "Complete genomic sequence of Pasteurella multocida Pm70."; Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 90
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B583448BA4E0DFD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EB34CEFF7737B93B CRC64;
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W. No. 0.0012;
Mismatches 47
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Pred. No. 0.0012;
0; Mismatches 4
                       family
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical UPF0269 protein PM1320.
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21:411-429(2000).
Belongs to the UPF0269
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InterPro; IPR007457; DUF495.
Pfam; PF04362; DUF495; 1.
PIRSF; PIRSF029827; DUF495; 1.
Hypothetical protein; Complete p SEQUENCE 90 AA; 10744 MW; B5
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TIGR; H10760; -. HAMAP; MF_00686; -; 1.

InterPro; IPR007457; DUF495.

Pfam; PF04362; DUF495; 1.

PIRSF; PIRSF029827; DUF495; 1

Complete proteome.

SEQUENCE 90 AA; 10582 MW;
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13; Conser
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les 13; Conser
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AE012353; ; MF_00686;
 SIMILARITY:
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XCC2419.
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10-OCT-2003
10-OCT-2003
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SEQUENCE FROM N.A.
STRAIN=RIMD 2210633 / Serotype O3:K6;
MEDLINE=22508454; PubMed=12620739;
Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomo Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimu Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
"Genome sequence of Vibrio parahaemolyticus: a pathogenic mech distinct from that of V. cholerae.";
                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fe entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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                                                                                                                              Vibrio vulnificus.
Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales,
Vibrionaceae, Vibrio.
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Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
NCBI_TaxID=670;
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                                                                                                                                                                                                                                 databases
                                                                                                                                                                                                                                                                                                                                        EMBL; AE016801; AA009940.1; -.
HAMAP; MF_00686; -; 1.
InterPro; IPR007457; DUF495.
Pfam; PF04362; DUF495; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 90 AA; 10614 MW; 7EA0CB75840A255C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                    S.S., Kim J.J., Moon Y.H.,
                                                                                                                                                                                                                       CMCP6
                                                                                                                                                                                                                                                                                                                                                                                                     Score 47; DB 1; Len
Pred. No. 0.0012;
                                                                                                                                                                                                                      "Complete genome sequence of Vibrio vulnificus
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ o
-!- SIMILARITY: Belongs to the UPF0269 family.
                                                                   10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical UPF0269 protein W11514.
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical UPF0269 protein VP2627.
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Rhee J.H., Kim S.Y., Chung
Choy H.E.;
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STRAIN=ATCC 33913 / NCPPB 528;

X MEDLINE=22022145; PubMed=12024217;

X da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

Alves L.M.C., do Amaral A.M., Estrolini M.C., Camargo L.E.A.,

Alves L.M.C., do Amaral A.M., Cardozo J., Chambergo F., Ciapina L.P.,

A cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos D.H.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira E.C., Tezza R.I.D.,

Trindade dos Santos M., Trantfi D., Teai S.M., White F.F.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

Trindade dos Santos M., Truffi D., Teai S.M., White F.F.,

Comparison of the genomes of two Xanthomonas pathogens with differing host specificities.";

Nature 417:459-463(2002).

Letter R. M. Nature 417:459-463(2002).

Letter R. M. Nature H.R. M. Belongs to the UpF0269 family.
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
NCBI_TaxID=340;
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A20D59535F0F9A1B CRC64;
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Belongs to the UPF0269 family
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Pred. No. 0.0012
; Mismatches
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InterPro; IPR007457; DUF495.
Pfam; PF04362; DUF495; 1.
Hypothetical protein; Complete SEQUENCE 90 AA; 10629 MW; P
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Similarity 23.6%;
13; Conservative
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                                                                                                                                                                                                                         symbiotic bacterium).
Bacteria; Gammaproteobacteria; Enterobacter:
Enterobacteriaceae; Buchnera.
NCBI_TaxID=118099;
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=TOkyo 1998;
MEDLINE=20445173; PubMed=10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa "Genome sequence of the endocellular bacterial symbiont of Buchnera sp. APS.";
Nature 407:81-86(2000).
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00B049027CF480BF CRC64;
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Pred. No. 0.0017;
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F14506B181DB19E5
                                                     Score 47; DB 1;
Pred. No. 0.0012;
0; Mismatches
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(Rel. 42, Last sequence update)
(Rel. 42, Last annotation update)
. UPF0269 protein NMA0419/NMB2021.
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(Rel. 40, Last sequence update)
(Rel. 42, Last annotation update)
UPF0269 protein BU553.
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HAMAP; MF_00686; -; 1.
InterPro; IPR007457; DUF495.
Pfam; PF04362; DUF495; 1.
PIRSF; PIRSF029827; DUF495; 1.
Hypothetical protein; Complete proteome SEQUENCE 77 AA; 9511 MW; 00B049027C
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InterPro; IPR007457; DUF495.
Pfam; PF04362; DUF495; 1.
PIRSF; PIRSF029827; DUF495; 1.
Hypothetical protein; Complete SEQUENCE 92 AA; 10645 MW; F
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Similarity 23.6%;
13; Conservative
                                                      Similarity 23.6%;
13; Conservative
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Hypothetical UPF026
NMA0419 OR NMB2021.
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Science 287:1809-1815(2000).

Science 287:1809-1815(2000).

-!- SIMILARITY: Belongs to the UPF0269 family.

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SEQUENCE FROM N.A.

STRAIN=22491 / Serogroup A / Serotype 4A;

STRAIN=22491 / Serogroup A / Serotype 4A;

STRAIN=22491 / Serogroup A / Serotype 4A;

MEDLINE=20222556; PubMed=10761919;

A Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,

A Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,

A Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,

A Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,

A Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

Mhitehead S., Spratt B.G., Barrell B.G.;

"Complete DNA sequence of a serogroup A strain of Neisseria

meningitidis Z2491.";

Nature 404:502-506(2000).
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STRAIN=MCS8 / Serogroup B;
MEDLINE=20175755; PubMed=10710307;
Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson Feisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.
Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.E.
Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,
Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.,
"Complete genome sequence of Neisseria meningitidis serogroup B st
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Neisseria meningitidis (serogroup A), and
Nėisseria meningitidis (serogroup B).
Bacteria, Proteobacteria, Betaproteobacteria, Neisseriales;
Neisseriaceae, Neisseria.
NCBI_TaxID=65699, 491;
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EMBL; AE002552; AAF42344.1; -.
TIGR; NMB2021; -.; 1.
HAMAP; MF 00686; -; 1.
InterPro; IPR007457; DUF495.
Pfam; PF04362; DUF495; 1.
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Hypothetical UPF0269 protei
PSPTO5343.
Pseudomonas syringae (pv. t
Bacteria; Proteobacteria; G
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                                  SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

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STRAIN=DC3000;

MEDLINE=22834015; PubMed=12928499;

Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,

Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,

Adwinn M.L., Dodson R.J., Deboy R.T., Durkin A.S., Kolonay J.F.,

Madupu R., Daugherty S., Brinkac L., Beanan M.J., Haft D.H.,

Nelson W.C., Davidsen T., Zafar N., Zhou L., Liu J., Yuan Q.,

Khouri H., Fedorova N., Tran B., Russell D., Berry K., Utterback T.,

A Nelson W.C., Cartinhour T.V., D'Ascenzo M., Deng W.-L., Ramos A.R.,

A Alfano J.R., Cartinhour S., Chatterjee A.K., Delaney T.P.,

Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X., Bender C.L.,

Myite O., Fraser C.M., Collmer A.,

"The complete genome sequence of the Arabidopsis and tomato pathogen

Pseudomonas syringae pv. tomato DC3000.";

Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186 (2003).

-!- SIMILARITY: Belongs to the UPF0269 family.
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STRAIN=MR-1;

MEDLINE=22297686; PubMed=12368813;

Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.

Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,

Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,

DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,

Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,

Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,

Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,

Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.;

"Genome sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis.";

Nat. Biotechnol. 20:1118-1123(2002).
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HAMAP; MF_00686; -; 1.
InterPro; IPR007457; DUF495.
Pfam; PF04362; DUF495; 1.
Pfam; PF04362; DUF495; 1.
Hypothetical protein; Complete proteome.
Hypothetical protein; Complete proteome.
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Pred. No. 0.0019;
); Mismatches 42;
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical UPF0269 protein SO3369.
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  Pseudomonas
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Alteromonadaceae; Shewanella
NCBI_TaxID=70863;
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23.6%;
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13; Conservative
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Pseudomonadaceae;
NCBI_TaxID=323;
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MEDLINE=22423060; PubMed=12534463;
Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes I.,
Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MARTVNCVHLNKEADGLDFQLYPGDLGKRIFDNISKEAWGLWQKKQTMLINEKKL
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=160488;
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0C802FD7163B75A2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42;
                                                                                                                                                                                                                                                                                      EMBL; AE015774; AAN56367.1; -.
TIGR; SO3369; -.
HAMAP; MF_00686; -; 1.
InterPro; IPR007457; DUF495.
Pfam; PF04362; DUF495; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 92 AA; 10742 MW; 3116B2E995289B86
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red. No. 0.002;
Mismatches 4.
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Hypothetical UPF0269 protein PP0285,
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Pred.
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TIGR; PP0285; -.
HAMAP; MF_00686; -; 1.
InterPro; IPR007457; DUF495.
Pfam; PF04362; DUF495; 1.
Hypothetical protein; Complete pisseQUENCE 90 AA; 10596 MW; OCI
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Best Local Similarity 23.6%;
Matches 13; Conservative
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MEDLINE=22297718; PubMed=12219091;
Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori
Aksoy S.;
                                                                                                                                                                                                                                                           ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wigglesworthia glossinidia brevipalpis.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales
Enterobacteriaceae, Wigglesworthia.
                                                                                                                                                                                 STRAIN=GMI1000;

STRAIN=GMI1000;

MEDLINE=21681879; PubMed=11823852;

Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

"Genome 15:497-502(2002).

-!- SIMILARITY: Belongs to the UPF0269 family.
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O
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical UPF0269 protein RSc1235.
RSC1235 OR RS02742.
Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria, Proteobacteria, Betaproteobacteria, Burkholderiaceae; Ralstonia.
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BA7FAD0032CB3C9B
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flies, Wigglesworthia glossinidia.";
Nat. Genet. 32:402-407(2002).
-!- SIMILARITY: Belongs to the UPF0269 family.
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Pred. No. 0.0032
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AL646063; CAD14937.1; -. HAMAP; MF_00686; -; 1. InterPro; IPR007457; DUF495. Pfam; PF04362; DUF495; 1. PIRSF; PIRSF029827; DUF495; 1. Hypothetical protein; Complete piseQUENCE 91 AA; 10321 MW; BA
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26.8%;
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                                                                                                                                    TaxID=305;
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MEDLINE=22421331; PubMed=12533478;

MEDLINE=22421331; PubMed=12533478;

Miyaki C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H.,

Miyaki C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H.,

A Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,

Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Tsai S.M.,

A Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,

Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.E.,

Marino C.L., Giglioti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,

Baia G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V.,

A da Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,

Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sassaki F.T., Sena J.A.D.,

de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G.,

A civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,

Kitajima J.P.,

"Comparative analyses of the complete genome sequences of Pierce's

disease and citrus variegated chlorosis strains of Xylella
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Pred. No. 0.0032;
); Mismatches
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Bacteriol. 185:1018-1026(2003).
- SIMILARITY: Belongs to the UPF0269 family
            Score 45; DB 1;
Pred. No. 0.0032
); Mismatches (
                                                                                                                                                                                                                          10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical UPF0269 protein PD0883.
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HAMAP; MF 00686; -; 1.
InterPro; IPR007457; DUF495.
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                                                                                                                                                                                                                                                                                                                                            Nitrosomonas europaea.
Bacteria, Proteobacteria, Betaproteobacteria, Nitrosomonadales
Nitrosomonadaceae, Nitrosomonas.
NCBI_TaxID=915;
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STRAIN=ATCC 19718 / IFO 14298;
MEDLINE=22586410; PubMed=12700255;
Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Lancthauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;
"Complete genome sequence of the ammonia-oxidizing bacterium a "Complete genome sequence of the ammonia-oxidizing bacterium abligate chemolithoautotroph Nitrosomonas europaea.";
J. Bacteriol. 185:2759-2773(2003).
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                                                   EMBL; AB063521; BAC24222.1; -.
HAMAP; MF 00686; -; 1.
InterPro; IPR007457; DUF495.
Pfam; PF04362; DUF495; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 78 AA; 9611 MW; A8793457C807891D
                                                                                                                                    Score 44; DB 1;
Pred. No. 0.0047
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UPF0269 protein NE0322.
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HAMAP; MF_00686; -; 1.
InterPro; IPR007457; DUF495.
Pfam; PF04362; DUF495; 1.
PIRSF; PIRSF029827; DUF495; 1
Hypothetical protein; Complet SEQUENCE 90 AA; 10267 MW;
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90 AA; 10267 MW;
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larity 30.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESQUENCE FROM N.A.

STRAIN=ATCC 15692 / PAO1;

MEDLINE=20437337; PubMed=10984043;

A Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., A Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., A Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";

I nature 406:959-964(2000).

-!- SIMILARITY: Belongs to the UPF0269 family.
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STRAIN=06:H1 / CFT073 / ATCC 700928;
MEDLINE=22388234; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
UPF0269 protein yggX.
YGX OR C3550.
Escherichia coli O6.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
                                                                                                                                                                                                                                           Pseudomonas aeruginosa.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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02BB6ECEBF7AEF39 CRC64;
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Pred. No. 0.0053
); Mismatches
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update
Hypothetical UPF0269 protein PA5148.
PA5148.
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InterPro; IPR007457; DUF495.
Pfam; PF04362; DUF495; 1.
PIRSF; PIRSF029827; DUF495; 1.
Hypothetical protein; Complete p: SEQUENCE 90 AA; 10625 MW; 021
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SPECIES=E.coli; STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
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SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."
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                                             This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMB the European Bioinformatics Institute. There are no restriuse by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-silor send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Bur. Blattner F.R., Plunkett G. III, Bloch C.A., Pode C.K., Mayhew Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose I
                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
UPF0269 protein yggX.

YGGX OR B2962 OR Z4307 OR ECS3838 OR SF2959 OR S3162.
Escherichia coli,
NCBI_TaxID=562, 83334, 623;
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D7C66C2A35E63692 CRC64;
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Science 277:1453-1474(1997).
  uropathogenic Escherichia coli.";
oc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002)
· SIMILARITY: Belongs to the UPF0269 family.
                                                                                                                                                                                                                                                               23;
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Pred. No. 0.0053;
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Mau B., Shao Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pathogenicity and O157.";
                                                                                                                   PARTIAL SEQUENCE OF 1-12.

SPECIES=E.coli; STRAIN=K12 / EMG2;

MEDLINE=97443975; PubMed=9298646;

Link A.J., Robison K., Church G.M.;

"Comparing the predicted and observed properties of proteins encoded in the genome of Escherichia coli K-12.";

Electrophoresis 18:1259-1313(1997).
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SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H., Yang J., Yang G., Wu H., Qu D., Dong Yang J., Yang F., Zhang X., Zhang J., Xang G., Wu H., Qu D., Dong Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S., Sun L., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
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SEQUENCE FROM N.A.

SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;

MEDLINE=22590274; PubMed=12704152;

Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,

Mei J., Goldberg M.B., Purland V., Venkatesan M.M., Deng W.,

A Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,

A Schwartz D.C., Blattner F.R.;

I "Complete genome sequence and comparative genomics of Shigella

I flexneri serotype 2a strain 2457T.";

Infect. Immun. 71:2775-2786(2003).
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Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia col: 0157:H7 and genomic comparison with a laboratory strain K-12." DNA Res. 8:11-22(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-10.
SPECIES=E.coli; STRAIN=K12;
MEDLINE=99085675; PubMed=9868784;
Wasinger V.C., Humphery-Smith I.;
"Small genes/gene-products in Escherichia coli K-12.";
FEMS Microbiol. Lett. 169:375-382(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ., Langen H.,
f Escherichia
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SPECIES=E.col;
MEDLINE=99420866; PubMed=10493123;
Fountoulakis M., Takacs M.-F., Berndt P., Lange "Enrichment of low abundance proteins of Eschenhydroxyapatite chromatography.";
hydroxyapatite chromatography.";
Electrophoresis 20:2181-2195(1999).
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EMBL; AE000378; AAC75999.1; -...
EMBL; AE005526; AAG58093.1; -...
EMBL; AE015308; AAN44440.1; -...
EMBL; AE016988; AAN44440.1; -...
PIR; A65082; A65082.
PIR; A65082; A65082.
PIR; A65082; A65082.
PIR; A65082; A65082.
HAMAP; MF_00686; -; 1...
InterPro; IPR007457; DUF495.
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EMBL; AL627277; CAD02936.1; -.
EMBL; AE016844; AAO70576.1; -.
StyGene; SG????; yggX.
HAMAP; MF 00686; -; 1.
InterPro; IPR007457; DUF495.
Pfam; PF04362; DUF495; 1.
PIRSF; PIRSF029827; DUF495; 1.
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SPECIES=S.typhi; STRAIN=CT18;

X MEDLINE=21534947; Pubmed=11677608;

A Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,

A Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,

A Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,

A Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,

A Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,

A Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,

A Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,

Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,

Mhitehead S., Barrell B.G.;

"Complete genome sequence of a multiple drug resistant Salmonella

T enterica serovar Typhi CT18.";

I Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720; MEDLINE=21534948; PubMed=11677609; McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                 10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
UPF0269 protein yggX.
YGGX OR STM3111 OR STY3266 OR T3024.
Salmonella typhimurium, and
Salmonella typhi.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Salmonella.
NCBI_TaxID=602, 601;
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                                                                             Length
                                                  D7C66C2A35E62402 CRC64;
                                                       Score 44; DB 1; Len
bred. No. 0.0053;
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- SIMILARITY: Belongs to the UPF0269 family.
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                                                                                                                       23 PXXXGXXXXXXXXXXXXXXXXXQTXLXNEXXL
                                                                                                                                               PGELGKRIYNEISKEAWAOWOHKQTMLINEKKL
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                                                  10821 MW;
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Pfam; PF04362; DUF495; 1.
PIRSF; PIRSF029827; DUF495; Complete proteome.
INIT_MET 0 0 SEQUENCE 90 AA; 10821 MW;
                                                                                   Similarity 30.3
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XAANISSES;

XA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,

SAANISSES;

RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Bappista C.S.,

RA Barros M.H., Bonacorsi B.D., Camargo L.B.A., Carraro D.M., Carrer H.

RA Coulton N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,

RA Facincani A.P., Ferreira A.J.S., Ferreira W.C.A., Ferro J.A.,

Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,

RA Facincani A.P., Jonana G.L., Ferreira W.C.A., Ferro J.A.,

RA Garnier M., Goldman M.H.S., Gomes S.L., Gruber A.,

RA Ho P.L., Hohelsel J.D., Junquelra M.L., Remper B.L., Kitajima J.P.,

RA Krieger J.E., Kiramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,

RA Machado M.A., Madeira A.M.B.N., Martins E.M.F., Marshado J.A.,

RA Marques M.V., Martins E.A.L., Martins E.M.F., Marino C.L.,

RA Marques M.V., Mascimento A.L.T.O., Netto L.E.S.,

RA Mono D.H., Nobrega F.G., Nunes L.R., Oliveira M.A.,

RA Moni A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,

RA G. Soliveira M.C., de Oliveira M.A.,

RA G. Sallveira J.F., Silvestri M.L.Z., Siqueira W.J., Tsulako M.H.,

RA da Silva A.C.R., da Silva A.M., Truffi D., Tsai S.M., Tsulako M.H.,

RA da Silva A.C.R., da Silva A.M., Verjovski-Almeida S., Vettore A.L.,

W. Ilada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,

W. Ilada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,

W. Ilada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,

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W. Ilada H., Valla Sluys M.A., Verjovski-Almeida S., Vettore A.L.,

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similarity: Belongs to the UPF0269 family.
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xylella.
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UPF0269 protein Xf1908.
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-!- SIMILARITY: Belongs to the UPF0269 family.
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                                                                                                                                                                                                                                                                                                            Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacter:
Enterobacteriaceae; Buchnera.
NCBI_TaxID=98794;
use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s.or send an email to license@isb-sib.ch).
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10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical UPF0269 protein BUsg535.
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InterPro; IPR007457; DUF495.
Pfam; PF04362; DUF495; 1.
Hypothetical protein; Complete SEQUENCE 90 AA; 10555 MW; E
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HAMAP; MF 00686; -; 1.
InterPro; IPR007457; DUF495.
Pfam; PF04362; DUF495; 1.
                                                                                                                      similarity 47.1%;
8; Conservative
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ID Y501 BUCBP
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**SEQUENCE FROM N.A.

**REDLINE=22426901; PubMed=12522265;

**A Van Ham R.C.H.J., Kamerbeek J., Palacios C., Rausell C., Abascal F.,

**A Van Ham R.C.H.J., Kamerbeek J., Vimenez L., Postigo M., Silva F.J.,

**BESCOLINE=22426901; PubMed=1252265;

**A Van Ham R.C.H.J., Kamerbeek J., Vimenez L., Postigo M., Silva F.J.,

**BESCOLINE C., Latorre A., Valencia A., Moran F., Moya A.;

**Bastolla U., Fernandez J.M., Jimenez L., Postigo M., Silva F.J.,

**A Bastolla U., Fernandez J.M., Jimenez L., Postigo M., Silva F.J.,

**A Bastolla U., Fernandez J.M., Jimenez L., Postigo M., Silva F.J.,

**A Bastolla U., Fernandez J.M., Jimenez L., Postigo M., Silva F.J.,

**A Bastolla U., Fernandez J.M., Jimenez L., Postigo M., Silva F.J.,

**A Bastolla U., Fernandez J.M., Jimenez L., Postigo M., Silva F.J.,

**A Bastolla U., Fernandez L., Valencia A., Moran F., Moya A.;

**A Bastolla U., Fernandez L., Valencia A., Moran F.J.,

**A Bastolla U., Fernandez L., Valencia A., Moran F.J.,

**A Bastolla U., Fernandez L., Valencia A., Moran F.J.,

**A Bastolla U., Fernandez L., Valencia A., Moran F.J.,

**A Bastolla U., Fernandez L., Valencia A., Moran F.J.,

**A Bastolla U., Fernandez L., Valencia A., Moran F.J.,

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**A Bastolla U., Fernandez L., Palacia A., Moran F.
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                                                                                                                                                                 (subsp. Baizongia pistaciae).
eria; Gammaproteobacteria; Enterobacteriales;
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Bacteria, Proteobacteria, Betaproteobacteria; Burkholderiales
Burkholderiaceae; Ralstonia.
NCBI_TaxID=510;
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01-NOV-1991 (Rel. 20, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Poly-beta-hydroxybutyrate polymerase (EC 2.3.1.-) (Poly(3-hydroxybutyrate) polymerase) (PHB polymerase) hydroxybutyrate) polymerase) (PHB polymerase) (PHA synthase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    biosynthesis in Alcaligenes
I characterization of the PHB
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HAMAP; MF_00686; -; 1.
InterPro; IPR007457; DUF495.
Pfam; PF04362; DUF495; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 87 AA; 10676 MW; C7270142539D1223 CRC64;
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MEDLINE=91100279; PubMed=1987116;
Schubert P., Krueger N., Steinbuechel A.;
"Molecular analysis of the Alcaligenes eutrophus poly(3-hydroxybutyrate) biosynthetic operon: ider
         sequence update) annotation update)
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(Rel. 42, Last sequence (Rel. 42, Last annotation UPF0269 protein bbp501.
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MEDLINE=89359357; PubMed=2670936;
Peoples O.P., Sinskey A.J.;
"Poly-beta-hydroxybutyrate (PHB) bioseutrophus H16. Identification and chapolymerase gene (phbC).";
J. Biol. Chem. 264:15298-15303(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Polyhydroxyalkanoic acid synthase)
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بط
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Bacteria; Proteobacteria; Gama
Enterobacteriaceae; Buchnera.
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ilarity 26.7%;
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BBP501.
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ID PHBC_ALCEU
AC P23608;
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outstation
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MATERIAL
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MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gammaproteobacteria; Enterobacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrictuse by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and feentities requires a license agreement (See http://www.isb-sib or send an email to license@isb-sib.ch).
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Pfam; PF00561; abhydrolase; 1.
PHB biosynthesis; Transferase; Acyltransferase.
PHB biosynthesis; Transferase; POTENTIAL.
ACT SITE 319 319 POTENTIAL.
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
42, Februarion update)
43, Froteobacteria; Gammaproteobacteria;
51, Froteobacteria; Escherichia.
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ed. No. 4.7;
Mismatches
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Pred.
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42.9%;
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EMBL; M64341; AAA21979.1;
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IPR000073;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                         STRAIN=0157:H7 / RIMD 0509952;

STRAIN=0157:H7 / RIMD 0509952;

MEDLINE=21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Tahami M., Tobe T.,

Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli

"Complete genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).

-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

-!- SIMILARITY: BELONGS TO THE YAIC / YFIN (E.COLI), YHCK (B.SUBTILIS)
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
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STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=977426617; Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Mayhew G.F., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
NCBI_TaxID=562;
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"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
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BEBC2286ADBAECB0 CRC64;
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Pred. No. 7.4;
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EMBL; AP002559; BAB36117.1; -.
PIR; F90965; F90965.
InterPro; IPR000160; GGDEF.
Pfam; PF00990; GGDEF; 1.
SMART; SM00267; DUF1; 1.
TIGRFAMS; TIGR00254; GGDEF; 1.
PROSITE; PS50887; GGDEF; 1.
Hypothetical protein; Transmembrance.
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                         "Genome sequence of enter
Nature 409:529-533(2001).
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428
564 AA;
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Best Local Similarity
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Mau B., Shao Y.;
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C P58994;

T 28-FEB-2003 (Rel. 41, Last sequence update)

T 28-FEB-2003 (Rel. 41, Last annotation update)

T 28-FEB-2003 (Rel. 41, Last annotation update)

T 28-FEB-2003 (Rel. 41, Last annotation update)

E Synthetase) (Gamma-ECS) (GCS).

S Synthetase) (Gamma-ECS) (GCS).

S Buchnera aphidicola (subsp. Schizaphis graminum).

S Buchnera aphidicola (subsp. Schizaphis graminum).

C Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriale

OC Enterobacteriaceae; Buchnera.

OX NCBI_TaxID=98794;
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                                  MEDLINE=97251358; PubMed=9097040;

Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isor Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura A Mizobuchi K., Mori H., T., Motomura K., Nakade S., Nakamura A Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;

Yamamoto Y., Horiuchi T.;

Yamamoto Y., Horiuchi T.;

"A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map.";

DNA Res. 3:379-392(1996).

-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

-!- SIMILARITY: BELONGS TO THE YAIC / YFIN (E.COLI), YHCK (B.SUE
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MEDLINE=22084549; PubMed=12089438;

MEDLINE=22084549; PubMed=12089438;

Tamas I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A. Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G. Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G. Science 296:2376-2379 (2002).

Science 296:2376-2379 (2002).

-! - CATALYTIC ACTIVITY: ATP + L-glutamate + L-cysteine = ADP phosphate + gamma-L-glutamyl-L-cysteine.

-! - PATHWAY: Glutathione biosynthesis; first step.
                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMB the European Bioinformatics Institute. There are no restriuse by non-profit institutions as long as its content i modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sior send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33; DB 1; Length 564; Pred. No. 7.4; 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                           or send an email ...

EMBL; AE000287; AAC75022.1; ALT_INIT.

EMBL; D90835; BAA15784.1; -.

ECOGENE; EG14040; yedQ.

InterPro; IPR000160; GGDEF.

Pfam; PF00990; GGDEF; 1.

SMART; SM00267; DUF1; 1.

TIGRFAMS; TIGR00254; GGDEF; 1.

TIGRFAMS; TIGR00254; GGDEF; 1.

TYPOTHETICAL protein; Transmembrane; Complete proteome.

TRANSMEM 20 40 POTENTIAL.

TRANSMEM 360 380 GGDEF.

TRANSMEM 360 380 GGDEF.
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PEGUINCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=972;

WADINE=21848401; PubMed=11859360;

WEDLINE=21848401; PubMed=1185, Basham D., Basham D., Bowman S., Gentlen T., Angels M., Marris D., Hilbert D., Odell C., Angels M., Standers M., Malsh S., Nobels D., Malter S., Angels M., Scheden S., Stevens K., Sharp S., Relton J., Simmonds M., Squares R., Squares S., Stevens K., Angles M., Scheder M., Whitehead S., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Maller-Auer S., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Maller-Auer S., Angles M., Rochet M., Galler-Auer S., Mocelle M., Galler-Auer S., Mocelle M., Cadieur S., Mocelle M., Galler-Auer S., Angles M., Rochet M., Galler-Auer S., Mocelle M., Mocelle M., Mocelle M., Mocelle M., Mocelle M., Mocelle M., 
                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SIMILARITY: Belongs to the glutamate--cysteine ligase
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HAMAP; MF_00578; -; 1.
InterPro; IPR007370; Glu_cys_ligase.
InterPro; IPR006334; Glut_cys_ligase.
Pfam; PF04262; glu_cys_ligase; 1.
TIGRFAMS; TIGR01434; glu_cys_ligase; 1.
Glutathione biosynthesis; Ligase; Complete proteome.
SEQUENCE 518 AA; 61250 MW; 53E76B05654807F3 CRC64;
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
NCBI_TaxID=4896;
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01-FEB-1996 (Rel. 33, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Hypothetical protein CIF5.11c in chromosome I
SPACIFS.11C.
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Pred. No. 11;
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                                            This SWISS-PROT entry is copyright. It is produced through a colbetween the Swiss Institute of Bioinformatics and the EMBL outhe European Bioinformatics Institute. There are no restricticuse by non-profit institutions as long as its content is imposified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.chor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                     EMBL; 268136; CAA92239.1; -.

R EMBL; 268136; CAA92239.1; -.

R PIR; T38084; T38084.

R InterPro; IPR008938; ARM.

InterPro; IPR003151; FAT.

InterPro; IPR001440; TPR.

InterPro; IPR001440; TPR.

IN Fam; PF02259; FAT; 1.

R Fam; PF02260; FAT; 1.

R Fam; PF02454; PI3 PI4 kinase; 1.

R Fam; PF00454; PI3 PI4 kinase; 1.

R ProxITE; PS00915; PI3 4 KINASE 1; FALSE NEG.

PROSITE; PS00916; PI3 4 KINASE 2; FALSE NEG.

PROSITE; PS00916; PI3 4 KINASE 3; 1.

RW HYPOTHETICAL PROTEIN TRANSFERSE; Kinase.

MAMAIN 3324 3655

PISK/PI4K.

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MEDLINE=97271300; PubMed=9126251;
Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood
Rohrmann G.F.;
"The sequence of the Orgyia pseudotsugata multinucleocar
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SIMILARITY: Belongs to the PI3/PI4-kinase family
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Transcription regulation.
SEQUENCE 211 AA; 24139
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MEDLINE=21534947; PubMed=11677608;

MEDLINE=21534947; PubMed=11677608;

A Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., A Baker C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., A Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., A Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

""Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";

In Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Bacteriol. 185:2330-2337(2003).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: BELONGS TO THE YAIC / YFIN (E.COLI), YHCK (B.SUBTILIS)
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=Ty2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains and CT18.";
                                                                                                                                                                                                                                                             SALTI
YEDQ SALTI
STANDARD; PRT; 567 AA.
Q8Z5R0;
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical protein yedQ.
YEDQ OR STY2194 OR T0891.
Salmonella typhi.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella.
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       Length 211
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EMBL; AE016837; AA068569.1; -.
InterPro; IPR000160; GGDEF.
Pfam; PF00990; GGDEF; 1.
SMART; SM00267; DUF1; 1.
TIGRFAMS; TIGR00254; GGDEF; 1.
PROSITE; PS50887; GGDEF; 1.
Hypothetical protein; Transmembrane; Complete proteome.
TRANSMEM 20 40 POTENTIAL.
TRANSMEM 357 377 POTENTIAL.
DOMAIN 425 560 GGDEF.
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ore 31; DB 1
ed. No. 8.4;
Mismatches
   Score 31;
Pred. No.
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                                                      2,
Similarity 35.7%;
5; Conservative
                                                                                                                                                                                  146
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133 WNWWGLTRTLLIHE
                                                                                                                    WXXWXXXOTXLXNE
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                                                                                                                                                                                            MEDLINE=95350630, PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C., "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                    ROLE IN RECYCLING CELL DIVISION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY).

CATALYTIC ACTIVITY: Cleavage of the beta-1,4-glycosidic bond between N-acetylmuramic acid and N-acetylglucosamine residues, thereby conserving the energy in a newly synthesized 1,6-anhydrobond in the muramic acid residue.
SUBCELLULAR LOCATION: Periplasmic (Potential).
SIMILARITY: Belongs to the transglycosylase slt family.
                                                                                                                    Gammaproteobacteria; Pasteurellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYTIC MUREIN
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                                                                     precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Periplasmic; Signal
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AND/OR
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774DDD3D38217CEE
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Putative soluble lytic murein transglycosylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PUTATIVE SOLUBLE 1
TRANSGLYCOSYLASE.
SLT-TYPE DOMAIN.
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Pred. No. 21;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        Science 269:496-512(1995).
-!- FUNCTION: MUREIN-DEGRADING ENZYME. MAY
OF MUROPEPTIDES DURING CELL ELONGATION
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InterPro; IPR008258; SLT dom.
InterPro; IPR000189; Transglyc_AS.
Pfam; PF01464; SLT; 1.
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Hydrolase; Glycosidase;
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                                                                                 SLT OR H10829.
Haemophilus influenzae.
Bacteria; Proteobacteria; Gamm
Pasteurellaceae; Haemophilus.
NCBI_TaxID=727;
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ilarity 35.3%;
Conservative
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PIR; C64097; C64097.
HSSP; P03810; 1QSA.
TIGR; H10829; -.
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Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                         FROM N.A
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593 A
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Pfam: PF01464
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ID YQJK_ECOLI
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(B.SUBTILIS)
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                                                          Gaps
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STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P. McClelland M., Sanderson K.E., Ali J., Dante M., Du F., Hou S., Layman E Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman E Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium LT2.";
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Hypothetical protein yedQ.
YEDQ OR STM1987.
Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteria
NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EME the European Bioinformatics Institute. There are no restriuse by non-profit institutions as long as its content impdified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sior send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ure 413:852-856(2001).
SUBCELLULAR LOCATION: Integral membrane protein (Potent
SIMILARITY: BELONGS TO THE YAIC / YFIN (E.COLI), YHCK (1
FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 570;
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                           Length
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InterPro; IPR000160; GGDEF.
Pfam; PF00990; GGDEF; 1.
SMART; SM00267; DUF1; 1.
TIGRFAMS; TIGR00254; GGDEF; 1.
PROSITE; PS50887; GGDEF; 1.
Hypothetical protein; Transmembrane; CCTRANSMEM 360 380 POTENTIAL.
DOMAIN 428 563 GCDEF
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POTENTIAL.
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ilarity 35.3%;
Conservative
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Similarity 35.3%;
6; Conservative
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nes 6; Conser
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P44888;
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Best Local S
Matches 6
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Matches
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SLT HAEIN ID SLT H AC P4488

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WEDLINE=21848401; PubMed=11859360;
WEDLINE=21848401; PubMed=11859360;
WEDLINE=21848401; PubMed=11859360;
Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Genles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgen G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mononey P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Mononey P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Rutter K., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Abeljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Abeljens I., Vanstreels E., Rieger M., Reinhardt R., Pohl T.M., A Gabel C., Fuchs M., Fritzc C., Holzer E., Mooset D., Hilbert H., Machutt R., Purnelle B., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimenz J., Sanchez M., del Rey F., Benito J., Ander M., Moodle W.R., Paulsen I., Potsburg S.L., Ander M., Machiller J., Jamer J., Sanchez M., del Rey F., Benito J., Marnstrong J., Porsburg S.L., Marnstrong J., Potsburg S.L., Revrutti L., Lowe T., McCombie W.R., Paulsen I., Potskin J., Potsburg S.L., Revrutti L., Lowe T., McCombie W.R., Paulsen I., Potskin J., Potsburg S.L., Revrutti L., Lowe T., McCombie W.R., Paulsen I., Potskin J., Potsburg S.L., Potskin J., Potskin J
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                                                                                                                                                                                                                                                                                                                                                                       Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                             ; Complete proteome. 489054F32965EDCF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ussery D., Barrell B.G., Nurse P.;
ince of Schizosaccharomyces pombe.";
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21;
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PIR; C69026; C69026.
InterPro; IPR000286; His_deacetyls;
Pfam; PF00850; Hist_deacetyl; 1.
PRINTS; PR01270; HDASUPER.
Hypothetical protein; Hydrolase; CiseQUENCE 331 AA; 36722 MW; 489
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Best Local Similarity 45.:
Matches 5; Conservative
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                           SIMILARITY:
                                                This SWISS-PROT
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yhew G.F.,
ose D.J.,
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                                                                                                                                                      Enterobacteriales;
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SEQUENCE FROM N.A.

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MEDLINE=98037514; PubMed=9371463;

MEDLINE=98037514; PubMed=9371463;

Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,

Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,

Addafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,

Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,

McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,

A Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;

McComplete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics.";

J. Bacteriol, 179:7135-7155(1997).

-!- FUNCTION: Putative deacetylase (By similarity).
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                                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;

MEDLINE=97426617; PubMed=9278503;

MEDLINE=97426617; PubMed=9278503;

A Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland A Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.

A Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.

Mau B., Shao Y.;

Mau B., Shao Y.;

Annual B., Shao Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 99
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sin; Complete proteome.
11811 MW; DAD56718FFAF4086 CRC64;
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@
                                                                                                                                                     Gammaproteobacteria;
13-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein yqjK.
YQJK OR B3100.
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Pred. No. 7;
2; Mismatches
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(Rel. 36, Last sequence up
(Rel. 42, Last annotation
protein MTH1194.
                                                                                                                             Escherichia coli.
Bacteria; Proteobacteria; Gamma;
Enterobacteriaceae; Escherichia
NCBI_TaxID=562;
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MTH1194.
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15-JUL-1998
10-OCT-2003
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ID YB94_METTH
AC O27262;
DT 15-JUL-1998
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Matches 4
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Thode G.,

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Proto-oncogene; DNA DOMAIN 90 373 SEQUENCE 479 AA;
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            ctions on
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; Galliformes; Phasianidae; Phasianinae;
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between the Swiss Institute of Bioinformatics and the EMB the European Bioinformatics Institute. There are no restriuse by non-profit institutions as long as its content imposified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sior send an email to license@isb-sior).
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                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Fibroblast;
MEDLINE=88283637; PubMed=3293999;
MEDLINE=88283637; PubMed=3293999;
Boulukos K.E., Pognonec P., Begue A., Galibert F., Gesquier Stehelin D., Ghysdael J.;
"Identification in chickens of an evolutionarily conserved ets-2 gene (c-ets-2) encoding nuclear proteins related to t products of the c-ets proto-oncogene.";
EMBO J. 7:697-705(1988).
-! SUBCELLULAR LOCATION: Nuclear.
-! SUBCELLULAR LOCATION: Nuclear.
-! SIMILARITY: Contains 1 pointed (PNT) domain.
                                                                                                                                     Length 418;
                                                                                                                                                         Indels
                                                                                                                 COlD2DE4466C03E1 CRC64;
                                                                                                                                                           12;
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Pred. No. 26;
0; Mismatches
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Last annotation updat
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PIR; S00386; TVCHE2.
HSSP; P14921; 2STT.
TRANSFAC; T00116; -.
InterPro; IPR000418; Ets.
InterPro; IPR002341; HSF_ETS.
InterPro; IPR003118; SAM_PNT.
Pfam; PF00178; Ets; 1.
Pfam; PF02198; SAM_PNT; 1.
PRINTS; PR00454; ETSDOMAIN.
SMART; SM00413; ETS; 1.
SMART; SM00413; ETS, 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.
                                                                                                                                                                                                                                                                                                                    ETS2.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; (
Archosauria; Aves; Neognathae;
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Ω
                                                                                                                 46357 MW;
                                                                      EMBL; 298763; CAB11491.1; -. PIR; T39230; T39230. GeneDB_SPOMbe; SPAC9G1.07; - Hypothetical protein. SEQUENCE 418 AA; 46357 MW
                                                                                                                                        21.6%;
                                                                                                                                                                                39 WXXWXXXQTXLXNEXXL
                                                                                                                                                                                                    WGSWVSSQDTSKNSSNL
                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                 Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                          01-MAR-1989 (Rel
01-MAR-1989 (Rel
16-OCT-2001 (Rel
C-ETS-2 protein.
                                                                                                                                                                                                                                                                                                                                                                        TaxID=9031;
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Local S
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collaboration
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-!- FUNCTION: Involved in nuclear migration during development and thereafter. Not required for centrosome attachment to the nucleus. Probably recruited to the nuclear membrane by unc-84. May participate to nuclear migration via its interaction with unc-84, which possibly disrupts the interaction between unc-84 and anc-1 and therefore frees the nucleus form the cytoskeleton and allows the nuclear migration to proceed.

-!- SUBCELLULAR LOCATION: Type IV membrane protein (Potential). The transmembrane domain associates with the nuclear envelope.
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IsoId=Q23064-3; Sequence=VSP_007084;
IsoId=Q23064-3; Sequence=VSP_007084;
TISSUE SPECIFICITY: Predominantly expressed in migrating hyp7 nuclei, First expressed at the nuclear envelope of migrating hyp7 nuclei, then, at the bean embryonic stage, it is expressed in hyp7 cells, then, at the bean embryonic stage, it is expressed in a procells and intestinal cells. In adults, it is expressed in a procells and intestinal cells. In adults, it is expressed in a variety of cell-types, including cells around the pharynx and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhabditoidea;
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                                                                                                             479;
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Nuclear protein.
POINTED.
ETS-DOMAIN.
91BCD5206972E867 CRC64;
                                                                                                              Length
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                                                                                                                                                                                                                                                                                                                                                                          UN83 CAEEL STANDARD; PRT; 1041 AM. Q23064; Q95WB6; 10-OCT-2003 (Rel. 42, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) 10-OCT-2003 (Rel. 42, Last annotation update) Nuclear migration protein unc-83 (Uncoordinated UNC-83 OR W01A11.3. Caenorhabditis elegans.
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Θ
                                                                                                                 1;
                                                                                                  DB 29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   da; Chromadorea;
Caenorhabditis.
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Mismatches
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                                                                                                                 Score 30;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND INTERACTION ... STRAIN=Bristol N2;
MEDLINE=21614706; PubMed=11748140;
MEDLINE=21614706; PubMed=11748140;
MEDLINE=21614706; PubMed=11748140;
MEDLINE=21614706; PubMed=11748140;
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DNA-binding; N
173 P
453 E
AA; 54540 MW;
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o the
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30.8%;
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Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
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                                                                                                                                         Similarity 30.8
4; Conservative
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STRAIN=Bristol N2;
Blanchard M., Bradshaw H
Submitted (JUL-1996) to
                                                                                                                                                                                                                                                         117 WLAWATNEFSLAN
                                                                                                                                                                                                              WXXWXXXQTXLXN
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Submitted (JUN-2002)
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STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., May B., Shao Y.;
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01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cell division inhibitor.
SULA OR SFIA OR B0958 OR Z1308 OR ECS1042.
Escherichia coli, and
Escherichia coli 0157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacterialenterobacteria; Escherichia.
NCBI_TaxID=562; 83334;
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                                                                                                                                                                                                                                                                                                Length 1041;
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                                                                                         EMBL; AF338767; AAL15621.1; -.
EMBL; U64852; AAB04966.2; -.
WormPep; W01A11.3; CE31077.
Nuclear protein; Transmembrane; Developmental protein;
Alternative splicing.
TRANSMEM 1005 1024 ANCHOR FOR TYPE IV MEMBRAN
                                                                                                                                                                        (POTENTIAL).

COILED COIL (POTENTIAL).

COILED COIL (POTENTIAL).

Missing (in isoform b).

/FTId=VSP 007083.

Missing (in isoform c).

/FTId=VSP 007084.
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Freudl R., Braun G., Honore N., Cole S.T.;
"Evolution of the enterobacterial sulA gene: a ccsystem encoding an inhibitor of cell division.";
Gene 52:31-40(1987).
                                                                                                                                                                                                                                                                                              ore 30; DB 1;
ed. No. 59;
Mismatches
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                                                                                                                                                                                                                                                                                              Score 30;
Pred. No. 5
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Beck E., Bremer E.;
"Nucleotide sequence of the gene ompA of
protein II of Escherichia coli K-12.";
Nucleic Acids Res. 8:3011-3024(1980).
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01-NOV-1988 (Rel. 09, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Cell division inhibitor.
SULA OR STM1071 OR STY1092 OR T1849.
Salmonella typhimurium, and
Salmonella typhi.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Salmonella.
NCBI TaxID=602, 601;
                                                                                                                                                                                              SEQUENCE FROM N.A.
SPECIES=S.typhimurium;
MEDLINE=87248093; PubMed=3297925;
Freudl R., Braun G., Honore N., Cole S.T.;
"Evolution of the enterobacterial sulA gene: a system encoding an inhibitor of cell division. Gene 52:31-40(1987).
                        RESULT 42
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ID SULA SALTY
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RECOLINE=87248093; PubMed=3297925;

Freudi R., Braun G., Honore N., Cole S.T.;

Freudi R., Braun G., Honore N., Cole S.T.;

Revolution of the enterobacterial sula gene: a component of the SOS

System encoding an inhibitor of cell division.";

Gene 52:31-40(1987).

Gene 52:31-40(1987).

-!- FUNCTION: SULA IS A COMPONENT OF THE SOS SYSTEM AND AN INHIBITOR

CELL DIVISION AND THE APPEARANCE OF LONG, NON-SEPTATE FILAMENTS.

THE EXPRESSION OF SULA IS REPRESSED BY LEXA PROTEIN. FTSZ SEEMS

TO BE THE TARGET OF SULA.

-!- SUBCELLULAR LOCATION: Inner membrane.

C. -!- MISCELLANEOUS: THE N-TERMINUS OF SULA PROTEIN MIGHT BE INVOLVED IN

RECOGNIZING THE CELL DIVISION APPARATUS.

-!- SIMILARITY: THE C-TERMINUS SHOWS SIMILARITY TO THE N PROTEIN OF
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conserved region.

Low PROTEIN BINDING SITE

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                                                 CONSERVED REGION.
LON PROTEIN BINDING
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                                                                                                                                                                                                                                                                                                      Enterobacter aerogenes (Aerobacter aerogenes).
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Enterobacter.
NCBI_TaxID=548;
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01-NOV-1988 (Rel. 09, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cell division inhibitor.
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Cell division; Septation; So Complete proteome.
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PIR; C29016; C29016.
InterPro; IPR004596; SulPfam; PF03846; SulA; 1.
TIGRFAMS; TIGR00623; SulCell division; Septation
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169 AA;
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169 AA;
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SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;

MEDLINE=22531367; PubMed=12644504;

Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,

Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;

"Comparative genomics of Salmonella enterica serovar Typhi strains Ty
and CT18.";

J. Bacteriol. 185:2330-2337(2003).

-!- FUNCTION: SULA IS A COMPONENT OF THE SOS SYSTEM AND AN INHIBITOR

OF CELL DIVISION. ACCUMULATION OF SULA CAUSES RAPID CESSATION OF
CELL DIVISION OF SULA IS REPRESSED BY LEXA PROTEIN. FTSZ SEEMS
TO BE THE TARGET OF SULA.
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SEQUENCE FROM N.A.

SPECIES=S.typhi; STRAIN=CT18;

MEDLINE=21534947; PubMed=11677608;

MEDLINE=21534947; PubMed=118;

MEDLINE=21534947; PubMed=118;

MEDLINE=21534947; PubMed=118;

Medline M.A., Pickard D., Wain J.

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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium LT2.";
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MISCELLULAR LOCATION: Inner membrane.
MISCELLANBOUS: THE N-TERMINUS OF SULA PROTEIN MIGHT BE INVOLVED RECOGNIZING THE CELL DIVISION APPARATUS.
SIMILARITY: THE C-TERMINUS SHOWS SIMILARITY TO THE N PROTEIN OF PHAGE LAMBDA.
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LON PROTEIN BINDING SITE
S -> T (IN REF. 1).
R -> A (IN REF. 1).
H -> L (IN REF. 1).
V; 3848A73595E5D176 CRC64;
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Viruses; dsRNA viruses; Reoviridae; Phytoreovirus
NCBI_TaxID=142803;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Nonstructural protein Pns10.
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Pred. No. 37;
2; Mismatches
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Arch. Virol. 130:201-208(1993).
-!- SIMILARITY: TO WOUND TUMOR VIRUS S10.
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Pred.
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InterPro; IPR008777; Phytoreo_Pns.
Pfam; PF05451; Phytoreo_Pns; 1.
Nonstructural protein.
SEQUENCE 353 AA; 39196 MW; AF6
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MEDLINE=93277380; PubMed=8503785;
                                                       EMBL; M16324; AAA27230.1; -.
EMBL; AE008746; AAL20004.1; -.
EMBL; AL627269; CAD08197.1; -.
EMBL; AE016840; AA069467.1; -.
PIR; B29016; B29016.
StyGene; SG10386; SulA.
InterPro; IPR004596; SulA.
PFam; PF03846; SulA; 1.
TIGRFAMS; TIGR00623; Sula; 1.
Cell division; Septation; SOS re
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MEDLINE=88089533; PubMed=3335833;
Omura T., Minobe Y., Tsuchizaki T.;
"Nucleotide sequence of segment S10 of the rice dwarf virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 353;
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5 -> Y (IN REF. 1).
4 -> V (IN REF. 1).
9F6D51F539758413 CRC64;
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(Rel. 15, Last sequence update)
(Rel. 40, Last annotation update)
1 protein Pns10.
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Mismatches
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Chu R., Zhang X., Pan N., Chen Z.;
"The cDNA cloning and nucleotide sequence nonstructural protein of rice dwarf virus Acta Bot. Sin. 35:115-120(1993).
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                                                            Ververse Rovers (85441; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence upda 16-OCT-2001 (Rel. 40, Last annotation up Nonstructural protein Pns10. S10. Rice dwarf virus (isolate Fujian) (RDV). Viruses; dsRNA viruses; Reoviridae; Phyt
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No.
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EMBL; U25671; AAA70094.1; -.
InterPro; IPR008777; Phytoreo Pns.
Pfam; PF05451; Phytoreo Pns.
Nonstructural protein.
CONFLICT 159 159 T -> I
CONFLICT 320 320 D -> H
CONFLICT 328 328 S -> Y
CONFLICT 335 AA; 39247 MW; 9F6D!
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Viruses; dsRNA viruses; Reoviridae;
NCBI_TaxID=142805;
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InterPro;
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Volchkov V., Volchkova V., Eckel C., Klenk H.D., Bouloy M.,
Leguenno B., Feldmann H.;
I "Emergence of subtype Zaire Ebola virus in Gabon.";
Virology 232:139-144(1997).

- J. SUBCELLULAR LOCATION: Secreted.

- J. SUBCELLULAR LOCATION: Secreted.

- J. PTM: Pre-sGP is N-glycosylated. This precursor is processed into mature sGP and delta-peptide by the host furin. Both cleavage fragments contain sialic acid, but only the delta-peptide is O-glycosylated (By similarity).

- J. RNA EDITING: Modified positions=295; Note=Partially edited. RNA editing at this position consists of an insertion of one adenine nucleotide (By similarity). The sequence displayed here is the small secreted glycoprotein, derived from the edited RNA. The unedited RNA gives rise to the full-length transmembrane

C -!- SIMILARITY: Belongs to the filloviruses glycoprotein family.
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16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Pre-small/secreted glycoprotein precursor (pre-sGP) [Contains:
Small/secreted glycoprotein (sGP); Delta-peptide].
GP.
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ЕМВЪ
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                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMI the European Bioinformatics Institute. There are no restriuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sior send an email to license@isb-sib.ch).
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viruses; Mononegavirales;
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                                                      datsumura T., Sano T., Ohshima K., Shikata E., sequence of rice dwarf virus genome segment Acad., B, Phys. Biol. Sci. 63:227-230(1987). RITY: TO WOUND TUMOR VIRUS S10.
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8C7EC0CB559C88D0 CRC64;
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Pred. No. 37;
2; Mismatches
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kova V., Eckel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ebola virus (strain Eckron-76)
Viruses; ssRNA negative-strand
Ebola-like viruses.
NCBI_TaxID=129000;
     . 69:227-231(1988)
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4; Conservative
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"Nucleotide
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MEDLINE=97329084; PubMed=9185597;

NEDLINE=97329084; PubMed=9185597;

NEDLINE=97329084; PubMed=9185597;

NEDLINE=97329084; PubMed=9185597;

NEDLINE=97329084; PubMed=9185597;

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Viruses; ssRNA negative-strand viruses; Mononegavirales; Filoviridae
Ebola-like viruses.
NCBI_TaxID=128947;
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N-LINKED (GLCNAC. . .) (POTENTIAL)
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16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Pre-small/secreted glycoprotein precursor (pre-sGP) [Contains: Small/secreted glycoprotein (sGP); Delta-peptide].
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POTENTIAL.
EMBL; U81161; AAC57993.1; -.
InterPro; IPR002561; Filo_glycop.
Pfam; PF01611; Filo_glycop; 1.
Glycoprotein; Signal; RNA editing
SIGNAL
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4; Conservative
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IPR002561; Filo
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A Sanchez A., Trappier S.G., Mahy B.W., Peters C.J., Nichol S.T.;
Sanchez A., Trappier S.G., Mahy B.W., Peters C.J., Nichol S.T.;
The virion glycoproteins of Ebola viruses are encoded in two reading frames and are expressed through transcriptional editing.";

I Proc. Natl. Acad. Sci. U.S.A. 93:3602-3607(1996).

-!- SUBCELLULAR LOCATION: Secreted.

-!- RNA EDITING: Modified positions consists of an insertion of one adenine nucleotide. The sequence displayed here is the small secreted glycoprotein, derived from the edited RNA. The unedited RNA gives rise to the full-length transmembrane glycoprotein family.

-!- SIMILARITY: Belongs to the filoviruses glycoprotein family.
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reading
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                                                                          (BY
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 ; Filo glycop; 1.
Signal; RNA editing.
1 32 POTENTIAL.
33 364 PRE-SMALL/SECRETED GLYCOPROTEIN SIMILARITY).
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; Filo glycop; î.
Signal; RNA editing.
1 32 POTENTIAL.
33 364 PRE-SMALL/SECRETED GLYCOPROTEIN
SIMILARITY).
                                                                                                                                                                                                                                                                                                                 364;
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Viruses; ssRNA negative-strand viruses; Mononegavirales
Ebola-like viruses.
NCBI_TaxID=128951;
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                                                                                                                                                                                                                                                                                                                 Length
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VSGP_EBOZS STANDARD; P66801; Q66819; Q9YMG3;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Pre-small/secreted glycoprotein precursor (pre-sGP)
Small/secreted glycoprotein (sGP); Delta-peptide].
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InterPro; IPR002561; Filo_glycop.
Pfam; PF01611; Filo_glycop; 1.
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Viruses; ssRNA negative-strand viruses; Mononegavirales; Filoviridae;
Ebola-like viruses.
NCBI_TaxID=128952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reading
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the host furin. Both cleavage
but only the delta-peptide is O-
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MEDLINE=20072964; PubMed=10603327;
Volchkova V.A., Klenk H.D., Volchkov V.E.;
Volchkova V.A., Klenk H.D., Volchkov V.E.;
"Delta-peptide is the carboxy-terminal cleavage fragment of the nonstructural small glycoprotein sGP of Ebola virus.";
Virology 265:164-171(1999).
-!- SUBCELLULAR LOCATION: Secreted.
-!- PTM: Pre-sGP is N-glycosylated.
-!- PTM: Pre-sGP is N-glycosylated.
pature sGP and delta-peptide by the host furin. Both cleavage fragments contain sialic acid, but only the delta-peptide is glycosylated.
-!- RNA EDITING: Modified_positions=295; Note=Partially edited.
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MEDLINE=94055391; PubMed=8237108;
Sanchez A., Kiley M.P., Holloway B.P., Auperin D.D.;
"Sequence analysis of the Ebola virus genome: organization, gelements, and comparison with the genome of Marburg virus.";
virus Res. 29:215-240(1993).
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MEDLINE=96195018; PubMed=8622982;
Sanchez A., Trappier S.G., Mahy B.W., Peters C.J., Nichol S.The virion glycoproteins of Ebola viruses are encoded in trames and are expressed through transcriptional editing.";
Proc. Natl. Acad. Sci. U.S.A. 93:3602-3607(1996).
         GLYCOPROTEIN
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P60170; 012421; 012717; Q66801; Q66819; Q9YMG3;
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Pre-small/secreted glycoprotein precursor (pre-sGP)
Small/secreted glycoprotein (sGP); Delta-peptide].
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Pred. No. 38;
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MEDLINE=96130181; PubMed=8553543;
Volchkov V.E., Becker S., Volchkova Vetesov S.V., Klenk H.D.;
"GP mRNA of Ebola virus is edited by T? and vaccinia virus polymerases.";
Virology 214:421-430(1995).
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                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PRE-SMALL/SECRETED GLYCOPROTEIN.
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percent of the mRNA isolated from infected cells is edited. editing at this position consists of an insertion of one ac nucleotide. The sequence displayed here is the small secret glycoprotein, derived from the edited RNA. The unedited RNI rise to the full-length transmembrane glycoprotein (AC 2055 SIMILARITY: Belongs to the filoviruses glycoprotein family.
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MEDLINE=97061201; PubMed=8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Naka
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura
Miyajima N., Hirosawa M., Sugiura M., Nasamoto S.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Y
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P77972;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2.9lycerate hydro-lyase).
ENO OR SLR0752.
Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
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2-phospho-D-glycerate
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EMBL; U31033; AAA96745.1; -..
EMBL; AF086833; AAD14584.1; -..
InterPro; IPR002561; Filo_glycop.
Pfam; PF01611; Filo_glycop; 1..
Glycoprotein; Signal; RNA editing.
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           SUBCELLULAR LOCATION: Cytoplasmic (By sim. SIMILARITY: Belongs to the enolase family
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1; Mismatches
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PIR; S76837; S76837.

HSSP; P56252; 1PDZ.

HAMAP; MF_00318; -; 1.

InterPro; IPR000941; Enclase.

Pfam; PF00113; enclase; 1.

Pfam; PF03952; enclase; 1.

PRODOM; PR00148; ENCLASE:

ProDom; PD000902; Enclase; 1.

TIGRFAMS; TIGR01060; enc; 1.

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Lyase; Glycolysis; Magnesium; Cc

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Q7x6m7 oryza sativ
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STRAIN=35000HP / ATCC 700724;
STRAIN=35000HP / ATCC 700724;
Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur Johnson L., Nguyen D., Wang J., Forst C., Hood L.;
"The complete genome sequence of Haemophilus ducreyi.";
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases EMBL; AE017156; AAP96716.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 94 AA; 11039 MW; BSA232C56DE93765 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Haemophilus ducreyi.
Haemophilus ducreyi.
Bacteria; Proteobacteria; Gammaproteobacteria; Parsteurellaceae; Haemophilus.
NCBI_TaxID=730;
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Pred. No. 0.0053
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Q83KM9
Q8YK01
Q8YK02
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Q9BLZ7
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Q7vkb6 haemophilus
Q7vh06 bordetella
Q7vvc4 bordetella
Q7vvc9 candidatus
Q8abb2 bacteroides
Q8abb2 bacteroides
Q9v3p1 drosophila
Q8ss09 encephalito
Q8ss09 encephalito
Q9ss09 encephalito
Q9bap8 homo sapien
Q9ey23 xanthomonas
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STRAIN=12822 / ATCC BAA-587;

X MEDLINE=22827954; PubMed=12910271;

A Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,

A Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

A Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,

A Chthman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

A Chillingworth T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabbinowitsch E., Rutter S., Sanders M., Squares S., Stevens K.,

Rabbinowitsch E., Rutter S., Sanders M., Squares S., Stevens K.,

A Sharp S., Simmonds M., Skelton J., Squares S., Stevens K.,

Comparative analysis of the genome sequences of Bordetella pertussis,

Bordetella parapertussis and Bordetella bronchiseptica.";

I Nat. Genet. 35:32-40(2003).

EMBL, BX640428; CAE37004.1; -.
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STRAIN=RBSO / ATCC BAA-588;

MEDLINE=22827954; PubMed=12910271;

Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N., Atrin B., Davis B., Quail M.A., Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I., Corlins M., Cronin A., Davis B., Quail M.A., Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I., Chillingworth T., Collins M., Cronin A., Davis P., Doggett J., A Celtwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K. Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price (Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K., Sharp S., Simmonds M., Skelton J., Squares S., Stevens Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;

"Comparative analysis of the genome sequences of Bordetella perture Bordetella parapertussis and Bordetella bronchiseptica.";

Nat. Genet. 35:32-40(2003).

EMBL; Bx640447; CAE33897.1; -.

R Hypothetical protein; Complete proteome.

SEQUENCE 90 AA; 10568 MW; 7187EA3FB0420388 CRC64;
                                                                            Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
NCBI_TaxID=518;
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NCBI_TaxID=519;
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STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;

RA
MEDLINE=22827954; PubMed=12910271;

RA
Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA
Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA
Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
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Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA
Achtman M., Atkin R., Saker S., Basham D., Bason N., Cherevach I.,
Reltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
Rabbinowitsch E., Rutter S., Barrell B.G., Maskell D.J.;
T. Comparative analysis of the genome sequences of Bordetella pertussis,
T. Bordetella parapertussis and Bordetella bronchiseptica.";
RMBL, BX640418; CAE42609.1;
RHBL, BX6410418; CAE42609.1;
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MEDLINE=22784745; PubMed=12886019;
Gil R., Silva F.J., Zientz E., Delmotte F., Gonzalez-Candelas F
Latorre A., Rausell C., Kamerbeek J., Gadau J., Hoelldobler B.,
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein yggX.
YGX OR BFL248.
Candidatus Blochmannia floridanus.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriale Enterobacteriaceae; ant endosymbionts; Candidatus Blochmannia.
NCBI_TaxID=203907;
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Pred. No. 0.024;
0; Mismatches 30;
                                                         Score 44; DB 16;
Pred. No. 0.024;
); Mismatches 30
Hypothetical protein; Complete proteome. SEQUENCE 90 AA; 10568 MW; 7187EA3FB0420388
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1 protein; Complete proteome.
90 AA; 10568 MW; 7187EA3FB0420388
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Similarity 26.8%;
11; Conservative
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Bacteria; Proteobacteria; I
Alcaligenaceae; Bordetella
NCBI_TaxID=520;
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BP2336.
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Hypothetical
SEQUENCE 90
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01-OCT-2003
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Q7VRG9;
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SEQUENCE FROM N.A.
STRAIN=V583 / ATCC
MEDLINE=22550857; F
SEQUENCE FROM N.A. STRAIN=Berkeley; MEDLINE=20196006;
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygot;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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STRAIN=VPI-5482 / ATCC 29148;
STRAIN=VPI-5482 / ATCC 29148;
MEDLINE=22550858; PubMed=12663928;
Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
Chiang H.C., Hooper L.V., Gordon J.I.;
"A genomic view of the human-Bacteroides thetaiotaomicron sy
Science 299:2074-2076(2003).
Science 299:2074-2076(2003).
Science 299:2074-2076(2003).
GO, GO:0005506; F:iron ion binding; IEA.
GO, GO:0004497; F:monooxygenase activity; IEA.
GO, GO:0004497; F:monooxygenase activity; IEA.
InterPro; IPR001273; Aaa hydroxylase.
InterPro; IPR000437; Prok_lipoprot_S.
ProDom; PD002559; Aaa hydroxylase; I.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; I.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; I.
SEQUENCE 634 AA; 70192 MW; A3A4F5328ECEF469 CRC64;
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Last sequence update)
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                                                                                                                      CRC64
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Last annotation update)
    van Ham R.C.H.J., Gross R., Moya A.;
"The genome sequence of Blochmannia floridanus: confireduced genomes.";
Proc. Natl. Acad. Sci. U.S.A. 100:9388-9393(2003)
EMBL; BX248585; CAD83319.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 79 AA; 9438 MW; AE44B1C2E10FBBED CRC
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                                                                                                                                                       Score 43; DB 16;
Pred. No. 0.036;
0; Mismatches 23
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Pred. No. 3.5;
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01-JUN-2003 (TrEMBLrel. 24, La
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Hypothetical protein.
BT0198.
Bacteroides thetaiotaomicron.
Bacteria; Bacteroidetes; Bacte
Bacteroidaceae; Bacteroides.
NCBI_TaxID=818;
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57
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01-MAY-2000 (TrEMBLrel. 13, C:
01-MAY-2000 (TrEMBLrel. 13, L:
01-JUN-2003 (TrEMBLrel. 24, L:
CG15327 protein.
CG15327.
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Similarity 35.3%;
6; Conservative
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hao Q., Zheng L.,
Zhu X., Smith H.O.,
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Lactobacillales; Enterococcaceae;
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PubMed=12663927
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Q831X6;
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O1-JUN-2003 (TrEMBLrel.
Hypothetical protein.
EF2369.
Enterococcus faecalis (
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Paulsen I.T., Banerjei L., Myers G.S.A., Nelson K.E., Seshadri R.,
Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
A Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,
Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson
Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.
"Role of mobile DNA in the evolution of vancomycin-resistant
I Enterococcus faecalis.";
Science 299:2071-2074(2003).
EMBL; AE016954; AA082091.1; -.
IGR; EF2369; -.
Hypothetical protein; Complete proteome.
SEQUENCE 172 AA; 20235 MW; 2F67564289B653E4 CRC64;
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STRAIN=GB-M1;

X MEDLINE=21576510; PubMed=11719806;

X Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,

Ratinka M.D., Duprat S., Cornillot E., Brottier P., Wincker P.,

A Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P.,

A Weissenbach J., Vivares C.P.;

"Genome sequence and gene compaction of the eukaryote parasite

"Genome sequence and gene compaction of the eukaryote parasite

"Genome sequence and gene compaction of the eukaryote parasite

"Genome Sequence and gene Compaction of the eukaryote parasite

"Genome Sequence and gene Compaction of the Enkaryote parasite

"Genome Sequence and gene Compaction of the Enkaryote parasite

"Genome Sequence and Gene Compaction of the Enkaryote parasite

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"Genome Sequence and Gene C.P."

"Genome Sequence C.P."

"Genome Sequen
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Encephalitozoon cuniculi.
Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
NCBI_TaxID=6035;
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                                                                                                                                                                                                                                              Length 172;
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                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                              OBSS09;
OBSS09;
O1-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
ADP_ribosylation factor-like GTP binding protein.
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fw; 6BA2DEA6BE00AB98
                                                                                                                                                                                                                                           Score 34; DB 16;
Pred. No. 8.2;
); Mismatches E
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28.6%;
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Submitted (APR-2001)
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SEQUENCE
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Best Local
Matches
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Q9HAP8
ID Q9HAP
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764 AA

PRT;

PRELIMINARY;

Q9HAP8

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                                                                                                              Vertebrata; Euteleostomi;
; Hominidae; Homo.
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Q9EY23;
Q9EY23;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 25, Last annotation update)
Putative acyl carrier protein.
Xanthomonas oryzae (pv. oryzae).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadaceae; Xanthomonas.
NCBI_TaxID=64187;
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Goel A.K., Rajagopal L., Nagesh N., Sonti R.V.;
"Xanthomonadin biosynthetic gene cluster from Xanthomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 132
                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE=Testis;
Cheng L.J., Li J.M., Sha J.H.;
"A novel gene related to testis development (PRTD).";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF311326; AAG33852.1; -.
SEQUENCE 764 AA; 80380 MW; 30077783C468EE6F CRC64;
                                                                                                                                                                                                                                                                                                                                                            Indels
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Q9HAP8;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Testis development protein PRTD.
Homo sapiens (Human).
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Last sequence update)
Last annotation update)
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Pred. No. 33;
1; Mismatches
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                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini;
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Submitted (AUG-2001) to the EMBL/GenBank
EMBL, AY010120; AAG38843.1; -.
InterPro; IPR006162; Ppantne S.
InterPro; IPR006163; Pp bind.
Pfam; PF00550; pp-binding; 1.
PROSITE; PS50075; ACP DOMAIN; 1.
PROSITE; PS00012; PHOSPHOPANTETHEINB; 1.
Phosphopantetheine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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ilarity 35.7%;
Conservative C
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Q8PF84;
Q1-OCT-2002 (TrEMBLrel. 2
01-OCT-2003 (TrEMBLrel. 2
01-OCT-2003 (TrEMBLrel. 2
Acyl carrier protein.
ACPC OR XAC4101.
Xanthomonas axonopodis (p
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Created) Last sequence update) Last annotation update)

PRT;

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REGURENCE FROM N.A.

SEQUENCE STOROUS PURMED-10731132,
Addras M.D. Celniker S.E. I. Holt R.A., Evans C.A., Gocayne J.D.,
Addras M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Addras M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Worthman J.K., Yandell N.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Harel R.G., Champe M., Peleifer B.D.,
Abril J.F., Agbayani A., An H.-J., Andrews Plannkoch C., Baldwin D.,
Abril J.F., Agbayani A., Barman B.P., Brandarl D., Bolshakov S.,
Beeson K.Y., Benos P.V., Berman B.P., Brandarl D., Bolshakov S.,
Beeson K.Y., Benos P.V., Berman B.P., Brandarl D., Bolshakov S.,
Beeson K.Y., Benos P.V., Berman B.P., Brandarl D., Bolshakov S.,
Brytis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.
Suttis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.
Buttis K.C., Busam D.A., Buller H., Cadieu E., Bolshakov S.,
Buttis K.C., Bolsam D.E., Downes M., Deng Z., Chann P., Brothes P.,
Buttis K.C., Busam D.E., Garg N.S., Gelbatt W.M., Glasser K.,
Abrich M.J., Harvey D., Heiman T.J., Hernandez J., Dietz S.M.,
R. Gode R. J., Gorrell J.H., Guz J., Ganner M., Glasser K.,
Aldali M., Aluston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Brytmel B.E., Kodira C.D., Kraft C., Kravitz S., Jang Y., Lin X.,
Liu X., Mattei B., McIncosh T.C., Morise J., Morise D., Dietz S.,
Briansko P., Lei Y., Leviteky A.A., Li J., Li J., Dietz S.,
Brasko P., Lei Y., Morshy B., Murphy B., Wallsein M., Shuse M., Shush T.,
Shue B.C., Siden Kiamon J.A., Nixok G.M., Schebeler F., Shen H.,
Shue B.C., Siden Kiamos I., Simpson M., Stupski M., Nelson D.,
Avirskas R., Pector C., Morris G., Wan D., Yari W. Shush H.,
Shue B.C., Stadaling A.C., Sandersen D.R., Wallsams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zhu X., Zhu X., Zhu X., Zhu X., Zhu S., Zhu X., Zhu S., Zhu
                                                                                                                                                                                     CG15256 protein.
CG15256 protein.
BG:DS04862.2 OR CG15256.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Enhvdroidea; Drosophilidae; Drosophila.
                                                                                                                                   (TrEMBLrel. 13, (TrEMBLrel. 13, 1 (TrEMBLrel. 16, 1
146 WYAWSDVQTVYAN 158
                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                       FROM N.A.
                                                                                                                                                                                                                                                                           Neoptera; Endopt
Ephydroidea; Dro
NCBI_TaxID=7227;
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01-MAR-2001
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                                                           PEQUENCE FROM N.N.

SEQUENCE FROM N.N.

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SEQUENCE FROM N.A.

A SILVA A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

A Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

A Silva A.C.R., Ferro J.A., Reinach F.C., Camargo L.E.A.,

A Localis R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

Carellis R.M., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

A Carellis R.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

Formighieri E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

A Catsuyama A.M., Kishi L.T., Madeira A.M.B.N., Martinez-Rossi N.M.,

A Catsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,

A Catsuyama A.M., Kishi L.T., Madeira A.M.B.N., Martinez-Rossi N.M.,

A Martins E.C., Machado M.A., Madeira A.M.B.N., Miyaki C.Y., Moon D.H.,

Martins E.C., Machado M.A., Manura R.E., Teixeira B.C., Tezza R.I.D.,

A Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

A Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

A Setubal J.C., Kitajima J.P.;

Comparison of the genomes of two Xanthomonas pathogens with differing

Not specificities ",

Nature 417.459-46312002,

REBL; AROSSO PPARITHEINE; 1.

RESPONDED PROBOBIS; PAMAB936.1; -

RESPONDED PROBOBIS; PAMAB936.1; -

RESPONDED PROBOBIS; PAMAB936.1; -

RESPONDED PROBOBIS; PAMAB936.1; -

RESPONDED PROBOBIS; PROBOMIN, 1.

RESPONDED PROBOMIN, 1.

RESPONDED PROBOMIN, 1.

RESPONDED PROBOMIN, 1.

RESPON
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     Gammaproteobacteria; Xanthomonadal
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eria; Spirochaetes; Spirochaetales; Spirochaetaceae;
_TaxID=58231;
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Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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Pred.
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17536 MW;
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"A phylogenetic analysis of a by flagellar genes.";
Submitted (JUL-2000) to the EEMBL; AB046578; BAB62244.1;
InterPro; IPR005648; FlgD.
Pfam; PF03963; FlgD; 1.
SEQUENCE 159 AA; 17536 MW;
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Σ
    Bacteria; Proteobacteria; Gam
Xanthomonadaceae; Xanthomonas
NCBI_TaxID=92829;
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illarity 38.5%;
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01-OCT-2002 (TrEMBL
Flagellar protein.
FLGD.
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STRAIN=ATCC700293;
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BG:DS04862.
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       FBgn0028880; BG:DS048
                                     Query Match
Best Local Similarity 41.2%;
Matches 7; Conservative
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WXXWXXXOTXLXN

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STRAIN=A3(2) / M145;
MINDLINE=21996410; PubMed=12000953;
MEDLINE=21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Seeger K., Saunders A., Woodward J., Barrell B.G., Parkhill J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence of the model actinomycete Streptomyces "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";

Nature 417:141-147(2002).

BEMBL; AL939108; CAB61610.1; -.

GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.

GO; GO:0006118; P:electron transport; IEA.

GO; GO:0006118; P:electron transport; IEA.

InterPro; IPR006090; Acyl-CoA dh C.

InterPro; IPR006091; Acyl-CoA dh N.

InterPro; IPR006092; Acyl-CoA dh N.

Pfam; PF02771; Acyl-CoA dh, 1.

Pfam; PF02771; Acyl-CoA dh N; 1.
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O9RJX2
ID O9RJX2
AC O9RJX2;
AC O9RJX2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2003 (TrEMBLrel. 25, Last annotation update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DF Putative acyl-CoA dehydrogenase.
GN SCO1198 OR SCG11A.29C.
OS Streptomyces coelicolor.
OS Streptomyces coelicolor.
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
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                                                                                                                                                                                                                                                                       to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  at of ordered cosmids and a detailed genetic and B Mb Streptomyces coelicolor A3(2) chromosome."; Microbiol. 21:77-96(1996).
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Pred. No. 30;
0; Mismatches
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SEQUENCE FROM N.A.
STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436
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llarity 54.5%;
Conservative
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Kinashi H., Hopwood D.A.;
"A set of ordered cosmids
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=A3(2);
Cerdeno A.M., Parkhill C
Submitted (NOV-1999) to
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STRAIN=A3(2);
Oliver K., Harris D.;
Submitted (NOV-1999) to
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ASTRAIN=Berkeley;
MEDLINE=99403001; PubMed=10471707;
Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
Celniker S., Rubin G.M.;
"An exploration of the sequence of a 2.9-Mb region of the genome of
                                                                                                                                                                                                                                                                                                                                                                                                                                         the industrial
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                                                                              Streptomyces avermitilis.

Streptomyces avermitilis.

Streptomycineae; Streptomycetaceae; Streptomyces.

Streptomycineae; Streptomycetaceae; Streptomyces.

NCBI_TaxID=33903;

[1]

PSEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;

MEDLINE=21477403; PubMed=11572948;

Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T., Shinose M., Shiba T., Sakaki Y., Hattori M.;

"Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary metabolites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OgnK86

OgnK86;

OgnK86;

Ol-OCT-2000 (TrEMBLrel. 15, Created)

Ol-OCT-2000 (TrEMBLrel. 15, Last sequence update)

Ol-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Hypothetical protein.

BG:DS04862.2 OR CG15256.

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophila.

NCB1_TaxID=7227;
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STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;

MEDLINE=22608306; PubMed=12692562;

Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuch Sakaki Y., Hattori M., Omura S.;

"Complete genome sequence and comparative analysis of microorganism Streptomyces avermitilis.";

Nat. Biotechnol. 21:526-531(2003).

EMBL; AP005049; BAC74851.1; -.

GO; GO:0005491; F:oxidoreductase activity; IEA.

GO; GO:0006118; P:electron transport; IEA.

InterPro; IPR006090; Acyl-CoA_dh_C.

InterPro; IPR006091; Acyl-CoA_dh_M.

Pfam; PF00770; Acyl-CoA_dh; 1.

Pfam; PF02770; Acyl-CoA_dh, 1.
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О
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    24, Created)
24, Last sequence update)
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Pred. No. 30;
0; Mismatches
01-JUN-2003 (TrEMBLrel. 24, Cres 01-JUN-2003 (TrEMBLrel. 24, Last 01-OCT-2003 (TrEMBLrel. 25, Last Putative acyl-CoA dehydrogenase FADE16 OR SAV7140.
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                                                                                       STRAIN=Berkeley;

C STRAIN=Berkeley;

A Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,

A Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,

A Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,

Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,

Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,

A Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,

A Stehi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,

A Zieran L.L., Rubin G.M.;

A Zieran L.L., Rubin G.M.;

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AE003413; AAF44947.1; -

B Flybase; FBgn0028880; BG:DS04862.2.

Hypothetical protein.

W Hypothetical protein.
                                                                                                                              R.G.,
Doyle C.M.,
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"Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli Kl2 and O157."; through comparison with genomes of Escherichia coli Kl2 and O157."; Nucleic Acids Res. 30:4432-4441(2002).

EMBL; AE015217; AAN43546.1; -.

InterPro; IPR000160; GGDEF.

Pfam; PF00990; GGDEF; 1.

SMART; SM00267; DUF1; 1.

TIGRFAMs; TIGR00254; GGDEF; 1.

TIGRFAMs; TIGR00254; GGDEF; 1.

Hypothetical protein; Complete proteome.

Hypothetical protein; Complete SadoaFEASDF CRC64; SEQUENCE 494 AA; 56208 Mw; 48D653A00AFEASDF CRC64;
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J., Dong J.,
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Chen S.,
Hou Y.,
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Orf, conserved hypothetical protein.
YEDQ OR SF2000.
Shigella flexneri.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
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u H., Qu D.,
Ding K., Cl
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STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Yang J., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Qiang B., Wer Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wer
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Pred. No. 37;
); Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
23.7%; Score 33; DB 5;
Best Local Similarity 41.2%; Pred. No. 34;
Matches 7; Conservative 1; Mismatches
 Drosophila melanogaster: the Adh region."; Genetics 153:179-219(1999).
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Best Local Similarity
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19

RESULT Q8FGJ7

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SEQUENCE FROM N.A.

A Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

TEXTENSIVE mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).

EMBL; AE016762; AAN80833.1;

InterPro; IPR000160; GGDEF.

SEMBL; SM00267; DUF1; 1.

SMART; SM00267; DUF1; 1.

SRART; SM00267; DUF1; 1.

SRART; SM00267; GGDEF; 1.

PROSITE; PS50887; GGDEF; 1.

PROSITE; PS50887; GGDEF; 1.

PROSITE; PS50887; GGDEF; 1.
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STRAIN=EGD-e / Serovar 1/2a;

KEDLINE=21537279; PubMed=11679669;

Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

A Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

A Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

A Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

Bentian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,

A Gautier L., Goebel W., Garcia-del Portillo F., Marrido P.,

A Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

A Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,

A Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

A Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;

"Comparative genomics of Listeria species.";

Comparative genomics of Listeria species.";

EMBL; AL591982; CAD00345:1; -.

R PIR; AC1358; AC1358.

R Listilist; LM002267; -.

R GO; GO:0005524; F:ATP binding; IEA.
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OBFGJ7;
OBFGJ7;
OBFGJ7;
O1-MAR-2003 (TrEMBLrel. 23, Created)
O1-MAR-2003 (TrEMBLrel. 24, Last sequence update)
O1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein yedQ.
YEDQ OR C2374.
Escherichia coli O6.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
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Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria
NCBI_TaxID=1639;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein lmo2267.
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Pred. No. 43;
0; Mismatches
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35.3%;
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6; Conservative
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SEQUENCE FROM N.A.
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STRAIN=68-1;
PubMed=12767982;
Hansen S.G., Strelow L.I., Franchi D.C., Anders D.G., Wong S.W.;
Hansen S.G., Strelow L.I., Franchi D.C., Anders Cytomegalovirus.";
"Complete Sequence and Genomic Analysis of Rhesus Cytomegalovirus.";
J. Virol. 77:6620-6636(2003).
EMBL; AY186194; AAP50679.1; -.
SEQUENCE 180 AA; 21556 MW; C9A61C4EA198DE0E CRC64;
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SECUDENCE.
STRAIN=BP-1;
MEDLINE=22225144; PubMed=12240834;
Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Kiyokawa C., Sugimoto M., Takeuchi C., Yamada M., Tabata S., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., "Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
DNA Res. 9:123-130(2002).
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                                                                                                               Length 1235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 180;
GO, GO:0004003; F:ATP dependent DNA helicase activity; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006281; P:DNA repair; IEA.
InterPro; IPR001064; Crystallin.
InterPro; IPR0010212; UvrD-helicase.
Pfam; PF00580; UvrD-helicase; 1.
PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 1235 AA; 142655 MW; E0329AD6F07E4716 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Created)

01-MAR-2003 (TrEMBLrel. 24, Last annotation update)

01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

Tll2396 protein.

TLL2396.

Synechococcus elongatus (Thermosynechococcus elongatus)

Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                  Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=103930;
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                                                                                                           DB 16;
89;
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                                                                                                              Score 33; DB
Pred. No. 89;
2; Mismatches
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Mismatches
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Pred. No.
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Local Similarity 30.8%;
les 4; Conservative
                                                                                                               23.7%;
larity 30.8%;
Conservative
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                                                                                                                                                                                                                                                                                                         cytomegalovirus
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Best Local Similarity
Matches 4; Conser
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Q7TFIS;
01-OCT-2003
01-OCT-2003
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Rh157.
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Q7TFI5
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Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
Entomopoxvirus B.
NCBI_TaxID=83191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
ORF MSV090 putative Molluscum contagiosum virus MC121L (vaccinia homolog, similar to GB:U60315.
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                                                                                                                               Length
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical pleckstrin homology (Fragment).
A530023E23RIK.
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Submitted (MAY-1998) to the EMBL/GenBank/DDBJ da
                                                                                      6395A1CADFC84975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
                                                                                                                             Score 32; DB 16;
Pred. No. 49;
; Mismatches
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Pred. No. 49;
1; Mismatches
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STRAIN=C57BL/6J; TISSUE=Aorta, and Vein;
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Tucson;
MEDLINE=99102612; PubMed=9847359;
Afonso C.L., Tulman E.R., Lu Z., Oma E
"The genome of Melanoplus sanguinipes
J. Virol, 73:533-552(1999).
                                                                                                                                                                                                                                                                                                                                                                   PRT;
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EMBL; AP005377; BAC09948.1; -
InterPro; IPR005338; UPF0075.
Pfam; PF03702; UPF0075; 1.
Complete proteome.
SEQUENCE 379 AA; 41365 MW;
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42842 MW;
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PIR; T28251; T28251.
InterPro; IPR004251; DUF230, Pfam; PF03003; DUF230; 1.
SEQUENCE 380 AA; 42842 MW;
                                                                                                                               Query Match
Best Local Similarity 30.8%;
Matches 4; Conservative
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Best Local Similarity 42.9%;
Matches 6; Conservative
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MEDLINE=97061201; PubMed=8905231;

Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,

Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,

Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,

A Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,

A Hosouchi T., Matsuno A., Muraki A., Nakazaki M., Naruo K., Okumura S.,

A Hosouchi T., Matsuno A., Muraki A., Nakazaki M., Naruo K., Okumura S.,

A Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,

Tabata S.;

Tabata M., Yasuda M.,

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                       the RIKEN Genome Exploration Research Group Phase I & II Teal analysis of the mouse transcriptome based on functional ann 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK040756; BAC30694.1; -.
EMBL; AK040756; BAC30694.1; -.
GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
InterPro; IPR001849; PH.
InterPro; IPR00159; RA_domain.
Pfam; PF00169; PH; 1.
Pfam; PF00188; RA; 1.
SMART; SM00233; PH; 1.
Hypothetical protein.
NON_TER 388 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 420;
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in; Complete proteome.
47851 MW; D617A38D9E8E958C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3BE39199396F511D CRC64;
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Bacteria; Cyanobacteria; Chroococcales; Synechocystis
NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 02, Created)
(TrEMBLrel. 02, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
| protein slr1865.
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Pred. No. 54;
1; Mismatches
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Similarity 35.7%;
5; Conservative
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SLR1865.
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01-FEB-1997
01-JUN-2003
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P73615
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097352
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                                                                                        Trypanosomatidae; Trypanosoma
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                                                                                                                       ESQUENCE FROM N.A.

KEDLINE=20017521; PubMed=10551359;

A Graham S.V., Terry S., Barry J.D.;

Graham S.V., Terry S., Barry J.D.;

Graham S.V., Terry S., Barry J.D.;

Typanosoma brucei.";

I Slycoprotein gene expression sites used in metacyclic stage

Trypanosoma brucei.";

Mol. Biochem. Parasitol. 103:141-154(1999).

ED Machine FROM N.A.

REDLINE=91081307; PubMed=2175429;

RATCHEWS K.R., Shiels P.G., Graham S.V., Cowan C., Barry J.D.;

Matthews K.R., Shiels P.G., Graham S.V., Cowan C., Barry J.D.;

RATCHEWS K.R., Shiels P.G., Graham S.V., Cowan C., Barry J.D.;

Matthews K.R., Shiels P.G., Graham S.V., Cowan C., Barry J.D.;

Nucleic Acids Res. 18:7219-7227(1990).

EMBL, AJ012199; CAA09956.1; --

SEQUENCE 518 AA; 55736 MW; 800D002074229468 CRC64;

SEQUENCE 518 AA; 55736 MW; RODD002074229468 LC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Bl16704 protein.
BLL6704.
Bradyrhizobium japonicum.
Bradyrhizobium japonicum.
Bradyrhizobiaceae; Bradyrhizobium.
Bradyrhizobiaceae; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ILTat 1.61 metacyclic VSG protein.
Trypanosoma brucei.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32; DB 5
Pred. No. 66;
0; Mismatches
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larity 35.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 WXXWXXXQTXLXNEXXL
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Best Local Similarity
Matches 6; Conser
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FROM N.A
    SEQUENCE
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Q8LRJO
ID Q8LRJ
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Q7X6M7
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SEQUENCE FROM N.A.

C TISSUE=Brain,

X MEDLINE=20181126; PubMed=10718198;

X MEDLINE=20181126; PubMed=10718198;

RA Nagase T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.;

XT "Prediction of the coding sequences of unidentified human genes.XVI.

XT "Prediction of the coding sequences of unidentified human genes.XVI.

XT The complete sequences of 150 new cDNA clones from brain which code

RT for large proteins in vitro.";

RE for large proteins in vitro.";

R
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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ABPB.
Streptococcus gordonii.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
NCBI_TaxID=1302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C4BB7B71F4CC9F59 CRC64;
                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                            O9P2F6
O9P2F6;
O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein KIAA1391 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O83YT7;
O83YT7;
O83YT7;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Pred. No. 1.4e+02
); Mismatches
      DB 77.
                             Score 32; DB Pred. No. 77; 0; Mismatches
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                             Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative
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38.5%;
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PROSITE; PS50238; RHOGAP;
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EMBL, AL662969; CAE04717.1; -. EMBL, AL731626; CAE05686.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Weng Q.J., Zhang L., Lu Y., Li Y., Li X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li T., Zhang Y.J., Lu Y., Li C., Li T., Zhang Y.J., Lu Y., Li C., Li T., Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H., Ren S.X., Lv G., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhu F.H., Hong G.F.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
STRAIN=38;
Xu D.-Q., Thompson J., Cisar J.O.;
"Genetic Loci for Coaggregation Receptor Polysaccharide Biosynthesis in Streptococcus gordonii 38.";
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY147912; AAN52126.1; -.
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
0SJNBA0043L24.5 protein (OSJNBB0002J11.13 protein).
OSJNBA0043L24.5 OR OSJNBB0002J11.13.
Oryza sativa (Rice).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Trache Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                       Length 232;
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ed. No. 52;
Mismatches 8
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Pred. No. 72;
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Pred. No.
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Best Local Similarity 38.5%;
Matches 5; Conservative
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Best Local Similarity
Matches 4; Conser
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42.9%;
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                                                                                                           WKSWKNAKTRVAN 411
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              Conservative
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Best Local Similarity
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QBLRJO;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
05-JNBa0016109.11 protein.
05-JNBA0016109.11.
05-JNBA0016109.11.
05-JNBA0016109.11.
05-JNBA0016109.11.
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STRAIN=VPI-5482 / ATCC 29148;
MEDLINE=22550858; PubMed=12663928;
MEDLINE=22550858; PubMed=12663928;
Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
Chiang H.C., Hooper L.V., Gordon J.I.;
"A genomic view of the human-Bacteroides thetaiotaomicron sym Science 299:2074-2076(2003).
EMBL; AE016936; AA07724.1; -.
GO; GO:0005945; C:6-phosphofructokinase complex; IEA.
GO; GO:0003723; F:RNA-binding; IEA.
GO; GO:0006096; P:Glycolysis; IEA.
GO; GO:0006278; P:RNA-dependent DNA replication; IEA.
InterPro; IPR000123; RNA_DNApolyms.
InterPro; IPR000477; RVTSe.
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1e+02;
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ed. No. 76;
Mismatches
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Pred. No.
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No.
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Bacteria; Bacteroidetes; Bacteroides
Bacteroidaceae; Bacteroides.
NCBI_TaxID=918;
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Best Local Similarity 35.7%;
Matches 5; Conservative
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Q8A412,
01-JUN-2003 (TrEMBLrel. 2
01-JUN-2003 (TrEMBLrel. 2
01-OCT-2003 (TrEMBLrel. 2
Reverse transcriptase.
BT2617.
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Best Local Similarity
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PRINTS;
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Q8A4I2
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C PROSCHATE.
C -I- INDUCTION: BY MANNITOL, ARABITOL AND SORBITOL. NOT INDUCED BY FRUCTOSE OR XYLULOSE.
-!- MISCELLANBOUS: THE MILY PROTEIN IS ENCODED BY THE MIL EFCKDYZ
C -!- MISCELLANBOUS: THE MILY PROTEIN IS ENCODED BY THE MIL EFCKDYZ
C -!- MISCELLANBOUS: THE MILY PROTEINS FOR THE UPTAKE AND UTILIZATION OF MANNITOL, ARABITOL AND SORBITOL.
C -!- SMILARITY: BELONGS TO THE FUCOKINASE / GLUCONOKINASE / GLYCEROKINASE / XYLULOKINASE PAMILY.
C -!- GLYCEROKINASE / XYLUCKINASE PAMILY.
C GLYCEROKINASE / XYLUCKINASE PAMILY.
C GLYCEROKINASE / XYLUCKINASE PAMILY.
C GLYCEROKINASE / XYLUCKINASE ACCIVILY; IEA.
C GCO016740; F: Kransferase activity; IEA.
C GCO016740; F: Kransferase activity; IEA.
C GCO016740; F: Kransferase activity; IEA.
C GCO016740; F: Krinase Betabolism; IEA.
C GCO016740; F: Krinase; Krinas
          Gaps
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STRAIN=DSM 50106;
MEDLINE=98121321; PubMed=9461423;
Bruenker P., Altenbuchner J., Mattes R.;
"Structure and function of the genes involved in mannitol, arabitand glucitol utilization from Pseudomonas fluorescens DSM50106.";
Gene 206:117-126(1998).
-!- CATALYTIC ACTIVITY: ATP + D-XYLULOSE = ADP + D-XYLULOSE 5-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pseudomonas fluorescens.
Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales,
Pseudomonadaceae, Pseudomonas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Xylulose kinase (EC 2.7.1.17) (Xylulokinase).
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7 ;
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Pred. No. 1.1e+02;
; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
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          Mismatches
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STRAIN=GMI1000;

X MEDLINE=21681879; PubMed=11823852;

A Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Arlat M., Eillault A., Brottier P., Camus J.C., Cannac S., Demange N., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Neissenbach J., Boucher C.A.;

R Meissenbach J., Boucher L., Bourge L., Boucher L., Boucher L., Boucher L., Boucher L., Boucher 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                 Pirellula
             Rhodopirellula baltica.
Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
Planctomycetaceae; Pirellula.
NCBI_TaxID=117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales
Burkholderiaceae; Ralstonia.
NCBI TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                    MEDLINE=22735913; PubMed=12835416;
Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.
Schlesner H., Amann R., Reinhardt R.;
"Complete genome sequence of the marine planctomycete Pirellu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Probable poly-beta-hydroxybutyrate polymerase transmembrane (EC 2.3.1.~).
PHBC OR RSC1631 OR RS03994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 553;
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                                                                                                                                                                                                                                                                                                                                         Score 31; DB 16; 1
Pred. No. 1.2e+02;
3; Mismatches 7;
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Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                598 AA.
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35.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 28.6%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           458
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Rest Local Similarity
                                                                                                                                                               FROM N.A.
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QBXYX5;
01-MAR-2002
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                                                                                                                                                               SEQUENCE
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Q8XYX5
В
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RESULT Q8G5P3

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STRAIN=NCC 2705;

X MEDLINE=22294977; Pubmed=12381787;

X Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,

A Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,

Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,

A Pridmore R.D., Arigoni F.;

I'The genome sequence of Bifidobacterium longum reflects its adaptation

T to the human gastrointestinal tract.";

Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).

EMBL; AB014719; AAN24773.1; -.

RGO; GO:0016747; F:transferase activity, transferring groups o. .; IEA.

InterPro; IPR002666; Acyl transf. 3.

R fam; PF01757; Acyl transf. 3.

Pfam; PF01757; Acyl transf. 3.

Hypothetical protein; Complete proteome.

W Hypothetical protein; Complete proteome.
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                                     (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
membrane protein with possible acetylase function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ·.
                                                                           Hypothetical membrane protein with possible acetylase function BL0962.
Bifidobacterium longum.
Bacteria; Actinobacteridae; Bifidobacterianes; Bifidobacteriaceae; Bifidobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the Amylase-Binding Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Li L.N., Scannapieco F.A.;

"Identification and Analysis of the Amylase-Binding Protestrom Streptococcus gordoni.";

Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF354648; AAK52749.1; -.

GO; GO:0016805; F:dipeptidase activity; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR005322; Peptidase U34.

InterPro; IPR000437; Prok lipoprot S.

Ffam; PF03577; Peptidase U34; 1.

PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.

SEQUENCE 652 AA; 72741 MW; C4092EFFE53DFD4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Streptococcus gordonii.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Streptococcus.
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Pred. No. 1.3e+02;
1; Mismatches 7;
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Pred. No. 1.4e+02;
2; Mismatches 8;
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Q93TK2;
01-DEC-2001 (TrEMBLrel. 19, Ca
01-DEC-2001 (TrEMBLrel. 19, La
01-OCT-2003 (TrEMBLrel. 25, La
Amylase-binding protein B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.3%;
ilarity 38.5%;
Conservative
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larity 28.6%;
Conservative
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                    FROM N.A.
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Q8G5P3
Q8G5P3;
01-MAR-2003
01-MAR-2003
                                                                                                                                                                                                                                                   SEQUENCE FR
STRAIN=NCC
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Q93TK2
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S.E., Craven B.,
Salzberg S.L.,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                    Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Oryza sativa chromosome 10 BAC OSJNBa0027P10 genomic sequence.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC084763; AAG60190.1; -.
HSSP; P35222; 1G3J.
Gramene; Q9AY55; -.
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                                                                                                                                                                                             Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
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The Rice Chromosome 10 Sequencing Consortium;
"In-depth view of structure, activity, and evolution
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=cv. Nipponbare;
Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins
Zismann V., Pai G., Bowman C.L., Fujíi C.Y., VanAken
Khalak H., Feldblyum T.V., Quackenbush J., White O.,
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Pred. No. 1.6e+02;
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InterPro; IPR001225; Armadillo.
InterPro; IPR001810; F-box.
InterPro; IPR007089; LRR cys.
InterPro; IPR008945; Skpi Skp2.
Pfam; PF00514; Armadillo seg; 6.
Pfam; PF00646; F-box; 1.
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79515 MW;
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Q9AY55;
Q1-JUN-2001 (TrEMBLrel. 17, C:
01-JUN-2001 (TrEMBLrel. 17, L:
01-OCT-2003 (TrEMBLrel. 25, L:
Putative arm repeat protein.
OSJNBA0027P10.11.
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[2]
SEQUENCE FROM N.A.
STRAIN=cv. Nipponbare;
Buell C.R., Wing R.A., McCor
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SMART; SM00256; FBOX; 1
PROSITE; PS50181; FBOX;
SEQUENCE 751 AA; 795.
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STRAIN=0157:H7 / RIMD 0509952;

STRAIN=0157:H7 / RIMD 0509952;

STRAIN=0157:H7 / RIMD 0509952;

MEDLINE=21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Ida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli

O157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).

EMBL; AR005539; AAG58233.1; -.

REMBL; AR005564; BAB37405.1; -.

REMBL; E85971; E85971.

REMBL; F91126; F91126.

Complete proteome.

Complete proteome.

SEQUENCE 99 AA; 11781 MW; C6B9170493DF4086 CRC64;
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SEQUENCE FROM N.A.
STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                  Orf, hypothetical protein.
Z4454 OR ECS3982.
Escherichia coli O157:H7.
Bacteria; Froteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=83334;
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Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases EMBL; AE017120; AAP55033.1; -. SEQUENCE 751 AA; 79514 MW; 2E33B5FEE4A26685 CRC64;
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Pred. No. 1.6e+02;
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Pred. No. 39;
2; Mismatches 8
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QBXAH2;

01-MAR-2002 (TrEMBLrel. 20,

01-MAR-2002 (TrEMBLrel. 20,

01-JUN-2003 (TrEMBLrel. 20,
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MEDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
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                                                                                                           STRAIN=06:H1 / CFT073 / ATCC 700928;
MEDLINE=22388234; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P. Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., St. Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.; "Extensive mosaic structure revealed by the complete genome st of uropathogenic Escherichia coli."; Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
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SEQUENCE FROM N.A.
SPECIES=S.typhi; STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D.,
Parkhill J., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaih
Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaih
Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.
YQJK OR C3858.
Escherichia coli O6.
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteria
Enterobacteriaceae, Escherichia.
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08.KGR1,
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 20, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein (Putative inner membrane protein)
T3151 OR YOJK OR STM3231 OR STY3411.
Salmonella typhi, and
Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobs
                                                                                                                                                                                                                                                                           PIR; E85971; E85971.
PIR; F91126; F91126.
Hypothetical protein; Complete proteome.
SEQUENCE 99 AA; 11781 MW; C6B9170493DF4086 CRC64;
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Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,

Reltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,

Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,

Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,

Whitehead S., Barrell B.G.;

"Complete genome sequence of a multiple drug resistant Salmonella

T "Complete genome sequence of a multiple drug resistant Salmonella

T enterica serovar Typhi CT18.";

Nature 413:848-852(2001).

REMBL; AE016844; AA070692.1; ..

EMBL; AE016844; AA070692.1; ..

EMBL; AL627278; CAD07755.1; ..

Hypothetical protein; Complete proteome.

SEQUENCE 99 AA; 11548 MW; 26F4194AE256CE35 CRC64;
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EMBL; AE015325; AAN44614.1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 99 AA; 11781 MW; 33B9020486DF4137 CRC64;
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MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
NCBI_TaxID=623;
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01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
83351.
Shigella flexneri.
Shigella flexneri.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Pred. No. 39;
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Mismatches
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JN-2003 (TrEMBLrel. 24, Last seq
JN-2003 (TrEMBLrel. 24, Last ann
conserved hypothetical protein.
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Pred.
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SEQUENCE FROM N.A
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Q83J19;
01-JUN-2003
01-JUN-2003
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Gallus.
NCBI_TaxID=9031;
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                    SEQUENCE FROM N.A.

STRAIN=2457T / ATCC 700930 / Serotype 2a;

STRAIN=22590274; PubMed=12704152;

MEDLINE=22590274; PubMed=12704152;

Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,

A Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,

A Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,

A Schwartz D.C., Blattner F.R.;

"Complete genome sequence and comparative genomics of Shigella

I flexneri serotype 2a strain 2457T.";

Infect. Immun. 71:2775-2786(2003).

EMBL; AE016989; AAP18428.1; -.

Hypothetical protein.

SEQUENCE 99 AA; 11781 MW; 33B90651D7DB1466 CRC64;
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ie; Mus.
                                                              ing A.,
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi,
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the RIKEN Genome Exploration Research Group Phase I & II "Analysis of the mouse transcriptome based on functional 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK019001; BAC25574.1; -.
MGD; MGI:1914665; 3321401G04Rik.
Hypothetical protein.
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Q918Q8,
Q918Q8,
Q160CT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Bone morphogenetic protein 7 (Fragment).
Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Archosauria; Aves; Neognathae; Galliformes; Phasian
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Last annotation update)
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ed. No. 39;
Mismatches 8;
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Pred. No. 48;
1; Mismatches
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Pred. No.
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01-MAR-2003 (TrEMBLrel. 23, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
Hypothetical protein (Fragment).
3321401G04RIK.
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STRAIN=C57BL/6J; TISSUE=Pancreas;
MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
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36.4%;
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Best Local Similarity 28.6%;
Matches 4; Conservative
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01-MAR-2003
01-JUN-2003
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SEQUENCE FROM N.A.

STAIN=306 / ATCC 13902 / XV 101;

STRAIN=306 / ATCC 13902 / XV 101;

MEDDLINE=22022145; PubMed=12024217;

da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

A cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

Faria J.B., Ferreira A.J.S., Ferreira R.C., Ferro M.I.T.,

A cicarelli R.M., Kishi L.T., Leite R.P., Lemos J.G.M., Lemos M.V.F.,

Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

Martins E.C., Meidanis J., Menck C.F.M., Myaki C.Y., Moon D.H.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

A Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

Setubal J.C., Katajima J.F.,

"Comparison of the genomes of two Xanthomonas pathogens with differing

"Tomature 417:459-463 (2002).

EMBL, AB011926, AAM37696.1; -.

Hypothetical protein, Complete proteome.

Hypothetical protein, Complete proteome.
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Xanthomonadaceae; Xanthomonas.
NCBI_TaxID=92829;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein XAC2851.
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Pred. No. 48;
0; Mismatches
SEQUENCE FROM N.A.

MEDLINE=20307867; PubMed=10848589;

Monroe D.G., Jin D.F., Sanders M.M.;

"Estrogen Opposes the Apoptotic Effects of Bo
7 on Tissue Remodeling.";

Mol. Cell. Biol. 20:4626-4634(2000).

EMBL; AF223970; AAF34758.1; -.

InterPro; IPR001111; TGFb_N.

Pfam; PF00688; TGFb_propeptide; 1.

NON TER 124 AA; 13794 MW; F70104D9196A42
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larity 38.5%;
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Best Local Similarity 35.7
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X MEDLINE=21085660; PubMed=11217851;

X Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konoo H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,

A Aizawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

A Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

A Radota K., Matsuda H.A., Ashburner M., Batalov S., Cosavant T.,

A Ruchl D., Lewis S., Matsuo V.V., Nikaido I., Pesologe G., Quackenbush J.,

Ruchl D., Lewis S., Matsuo W., Aono H., Baldarelli R., Barsh G.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Byons P., Marchlonni L., Mashlana J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hayashizaki Y.,

Hayashizaki Y.,

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Hayashizaki Y.,

"Luch Mandal M., Radisaki Y.,

"Luch M. Massarelli M., Radisaki M
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
NCBI TaxID=10090;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                              the RIKEN Genome Exploration Research Group Phase I & II "Analysis of the mouse transcriptome based on functional 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AK004097; BAC25066.1; -.
MGD; MGI:1914665; 3321401G04Rik.
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               Q8BTD3,
Q8BTD3;
01-MAR-2003 (TrEMBLrel, 23, Created)
01-MAR-2003 (TrEMBLrel, 23, Last sequence update)
01-JUN-2003 (TrEMBLrel, 24, Last annotation update)
Hypothetical protein (Fragment).
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01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
4930469G21Rik protein.
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                                                                                 Gaps
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                                                                                                                                                                                                                     01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to Dictyostelium discoideum (Slime mold). prenyl cysteine carboxyl methyltransferase.
Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
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Methyltransferase; Transferase. SEQUENCE 235 AA; 27177 MW; CCDCAA6C8AF85014 CRC64;
BAB29884.1; -.
1; 4930469G21Rik.
1A; 21841 MW; C445DF77CDEE361B CRC64;
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